SEQUENCE LISTING

Dagonion Divino
<pre><110> University of Utah Research Foundation Cognetix, Inc. Olivera, Baldomero M. McIntosh, J. Michael Garrett, James E. Watkins, Maren Cruz, Lourdes J. Shon, Ki-Joon Jacobsen, Richard Jones, Robert M. Cartier, G. Edward Shen, Greg S. Wagstaff, John D.</pre>
<120> Mu-Conopeptides
<130> 2314-280
<150> US 09/010,009 <151> 2001-07-23
<150> US 60/277,270 <151> 2001-03-21
<150> US 60/264,319 <151> 2001-01-29
<150> US 60/245,157 <151> 2000-11-03
<150> US 60/219,619 <151> 2000-07-21
<160> 520
<170> PatentIn version 3.0
<210> 1 <211> 280 <212> DNA <213> Conus arentus
<400> 1
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttcttga ccatctgtat 6
gettetgttt eccettaetg etetteeget ggatggggat eaacetgeag acegaeetge 12
agagegtatg caggaegaet ttataaetga geateateee etgtttgate etgteaaaeg 18
gtgttgcgag aggccatgca acataggatg cgtaccttgt tgttaatgac cagctttgtc 24
atcgcggcct catcaagcga ataagtaaaa cgattgcagt 28
<210> 2 <211> 67 <212> PRT <213> Conus arentus
<400> 2 Met Met Ser Lys Leu Gly Val Phe Leu Thr Ile Cys Met Leu Leu Phe 1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro

20 25 30 Ala Glu Arg Met Gln Asp Asp Phe Ile Thr Glu His His Pro Leu Phe Asp Pro Val Lys Arg Cys Cys Glu Arg Pro Cys Asn Ile Gly Cys Val Pro Cys Cys <210> 3 <211> 14 <212> PRT <213> Conus arentus <220> <221> PEPTIDE <222> (1)..(14)<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5 an d 12 is Pro or Hyp <400> 3 Cys Cys Xaa Arg Xaa Cys Asn Ile Gly Cys Val Xaa Cys Cys 10 <210> <211> 244 <212> DNA <213> Conus atlanticus <400> 4 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccactt 60 actgctcttc cgctggatga agatcaaccg gtacaccgac ctgcagagcg tatgcaggac 120 atttcatctg atcaacatct cttctttgat ctcatcaaac ggtgctgcga gttgccatgc 180 gggccaggct tttgcgtccc ttgttgctga catcaataac gtgttgatga ccaactttct 240 cgag 244 <210> <211> 69 <212> PRT <213> Conus atlanticus <400> 5 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Val His Arg Pro Ala Glu Arg Met Gln Asp Ile Ser Ser Asp Gln His Leu Phe Phe Asp Leu Ile Lys Arg Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe 55 50 Cys Val Pro Cys Cys

<210> 6

```
<211>
       1.5
<212>
       PRT
<213>
       Conus atlanticus
<220>
<221>
       PEPTIDE
<222>
       (1)..(15)
<223>
       Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 8
        and 13 is Pro or Hyp
<400> 6
Cys Cys Xaa Leu Xaa Cys Gly Xaa Gly Phe Cys Val Xaa Cys Cys
                                     10
                                                         15
<210>
<211>
       310
<212>
       DNA
<213>
       Conus aurisiacus
<400> 7
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgttt
                                                                        60
gcttctgttt ccccttactg ctcttccgat ggatggagat caatctgtag accgacctga
                                                                       120
agagcgtatg caggacgaca tttcatctga gcagcatccc ttgtttaatc agaaaagaat
                                                                       180
gtgttgcggc gaaggccgga aatgccccag ctatttcaga aacagtcaga tttgtcattg
                                                                       240
ttgttaaatg acaacgtgtc gatgaccaac ttcgttatca cgactaatga ataagtaaaa
                                                                       300
cgattgcagt
                                                                       310
<210>
       8
       74
<211>
<212>
       PRT
<213>
       Conus aurisiacus
<400>
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro
Glu Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Leu Phe
Asn Gln Lys Arg Met Cys Cys Gly Glu Gly Arg Lys Cys Pro Ser Tyr
Phe Arg Asn Ser Gln Ile Cys His Cys Cys
<210>
       9
       22
<211>
<212>
      PRT
<213> Conus aurisiacus
<220>
<221>
       PEPTIDE
<222>
       (1)..(22)
<223>
       Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 i
       s Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr,
```

di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

```
<400> 9
Met Cys Cys Gly Xaa Gly Arg Lys Cys Xaa Ser Xaa Phe Arg Asn Ser
Gln Ile Cys His Cys Cys
<210>
       10
<211>
       257
<212>
       DNA
<213>
       Conus aurisiacus
<400> 10
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtttgcttct gtttcccctt
                                                                       60
actgctcttc cgatcgatgg agatcaatct gtagaccgac ctgcagagcg tatgcaggat
                                                                      120
gacatttcat ctgagcagca tcgcttgttc aatcagaaaa gaaggtgctg ccggtggcca
                                                                      180
tgcccccgac aaatcgacgg tgaatattgt ggctgttgcc ttggatgata accgtgttga
                                                                      240
tgaccaactt tctcgag
                                                                      257
<210>
       11
<211>
       75
<212>
       PRT
<213>
       Conus aurisiacus
<400> 11
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
Leu Phe Pro Leu Thr Ala Leu Pro Ile Asp Gly Asp Gln Ser Val Asp
Arg Pro Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Arg
Leu Phe Asn Gln Lys Arg Arg Cys Cys Arg Trp Pro Cys Pro Arg Gln
Ile Asp Gly Glu Tyr Cys Gly Cys Cys Leu Gly
<210>
       12
<211>
<212>
       PRT
<213>
      Conus aurisiacus
<220>
<221>
       PEPTIDE
<222>
       (1)..(19)
<223>
       Xaa at residue 13 is Glu or gamma-carboxy Glu; Xaa at residue 5 a
       nd 7 is Pro or Hyp; Xaa at residue 4 is Trp or Bromo Trp; Xaa at
       residue 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho
       -Tyr or O-phospho-Tyr
<400> 12
Cys Cys Arg Xaa Xaa Cys Xaa Arg Gln Ile Asp Gly Xaa Xaa Cys Gly
Cys Cys Leu
```

```
<211>
       262
<212>
       DNA
<213>
       Conus aurisiacus
<400> 13
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt
                                                                        60
actgcttttc cgatggatgg agatcaacct gcagaccaac ctgcagatcg tatgcaggac
                                                                      120
gacatttcat ctgagcagta tcccttgttt gataagagac aaaagtgttg cactgggaag
                                                                      180
aaggggtcat gctccggcaa agcatgcaaa aatctcaaat gttgctctgg acgataacgt
                                                                      240
gttgatgacc aactttctcg ag
                                                                      262
<210>
       14
<211>
       78
<212>
       PRT
<213>
       Conus aurisiacus
<400> 14
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
Leu Phe Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp
            20
Gln Pro Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro
Leu Phe Asp Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys
Ser Gly Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
<210>
       15
<211>
       23
<212>
       PRT
<213> Conus aurisiacus
<220>
<221>
      PEPTIDE
<222>
      (1)..(23)
      Xaa at residue 1 is Gln or pyro-Glu
<400>
Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
Lys Asn Leu Lys Cys Cys Ser
<210>
       16
<211>
       232
<212>
       DNA
<213>
      Conus aurisiacus
<400> 16
ggatccatga tgtctaaact gggagtcttg ctgaccatct gtctgcttct gtttccactt
                                                                       60
actgctgttc cgctggatgg agatcaacct ctagaccgac acgcggagcg tatgcatgat
                                                                      120
ggcatttcac ctaaacgcca tccctggttt gatcccgtca aacggtgttg caaggtgcaa
```

```
tgcgagtctt gcaccccttg ttgctaacgt gttgatgacc aactttctcg aq
                                                                      232
<210>
       17
<211>
       68
<212>
       PRT
      Conus aurisiacus
<213>
<400> 17
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Leu Asp
            20
Arg His Ala Glu Arg Met His Asp Gly Ile Ser Pro Lys Arg His Pro
Trp Phe Asp Pro Val Lys Arg Cys Cys Lys Val Gln Cys Glu Ser Cys
Thr Pro Cys Cys
<210> 18
<211>
      13
<212>
      PRT
<213> Conus aurisiacus
<220>
      PEPTIDE
<221>
<222>
      (1)..(13)
<223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 11 i
       s Pro or Hyp
<400> 18
Cys Cys Lys Val Gln Cys Xaa Ser Cys Thr Xaa Cys Cys
<210> 19
<211>
      241
<212> DNA
<213> Conus bandus
<400> 19
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtatgcttct gtttccctc
                                                                       60
actgctcttc cgatggatgg agatcaacct gcagaccgac ctgcagagcg tagtcaggac
                                                                      120
gtttcatctg aacagcatcc cttgtttgat cccgtcaaac ggtgttgcaa ctggccatgc
                                                                      180
tccatgggat gcatcccttg ttgctactat taataacgtg ttgatgacca actttctcga
                                                                      240
                                                                      241
<210>
       20
<211>
       70
      PRT
<212>
<213>
      Conus bandus
<400> 20
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Met Leu
                                    10
Leu Phe Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp
            20
                                25
                                                     30
```

```
Arg Pro Ala Glu Arg Ser Gln Asp Val Ser Ser Glu Gln His Pro Leu
Phe Asp Pro Val Lys Arg Cys Cys Asn Trp Pro Cys Ser Met Gly Cys
Ile Pro Cys Cys Tyr Tyr
<210>
       21
<211>
       16
<212>
       PRT
     Conus bandus
<213>
<220>
<221>
      PEPTIDE
<222>
       (1)..(16)
      Xaa at residue 5 and 12 is Pro or Hyp; Xaa at residue 4 is Trp or
<223>
       bromo-Trp; Xaa at residue 15 and 16 is Tyr, 125I-Tyr, mono-iodo-
       Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400> 21
Cys Cys Asn Xaa Xaa Cys Ser Met Gly Cys Ile Xaa Cys Cys Xaa Xaa
                                    10
<210>
       22
<211>
       298
<212>
       DNA
<213>
      Conus betulinus
<400> 22
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccttctqtct
                                                                       60
gettetgttt eccetgactg etetteeget ggatgaagat caacetgeag accqaectge
                                                                      120
agagegtatg caggacattt catetgaaca geatecettg tttgateecg teaaacggtg
                                                                      180
ttgcgaattg ccatgccatg gatgcgtccc ttgttgctgg ccttaataac gtgtggatga
                                                                      240
ccaactgtgt tatcacggcc acgtcaagtg tctaatgaat aagtaaaatg attgcagt
                                                                      298
<210>
       23
<211>
       67
<212>
      PRT
<213> Conus betulinus
<400> 23
Met Met Ser Lys Leu Gly Val Leu Leu Thr Phe Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
Ala Glu Arg Met Gln Asp Ile Ser Ser Glu Gln His Pro Leu Phe Asp
Pro Val Lys Arg Cys Cys Glu Leu Pro Cys His Gly Cys Val Pro Cys
                        55
                                            60
Cys Trp Pro
65
<210>
       24
<211>
       15
<212>
       PRT
<213>
      Conus betulinus
```

```
<220>
       PEPTIDE
<221>
<222>
       (1)..(15)
       Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 1
       1 and 15 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Trp
<400> 24
Cys Cys Xaa Leu Xaa Cys His Gly Cys Val Xaa Cys Cys Xaa Xaa
                                     10
<210>
       25
<211>
      298
<212>
      DNA
<213>
      Conus betulinus
<400>
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccttctgtct
                                                                       60
gcttctgttt cccctgactg ctcttccgct ggatgaagat caacctgcag accgacatgc
                                                                      120
agagogtatg caggacattt cacctgaaca gcatccctcg tttgatcccg tcaaacggtg
                                                                      180
ttgcgggctg ccatgcaatg gatgcgtccc ttgttgctgg ccttcataac gtgtggacga
                                                                      240
ccaactttgt tatcacggcc acgtcaagtg tctgatgaat aagtaaaacg attgcagt
                                                                      298
<210>
       26
<211>
       68
<212>
       PRT
<213>
      Conus betulinus
<400> 26
Met Met Ser Lys Leu Gly Val Leu Leu Thr Phe Cys Leu Leu Phe
                                    10
Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg His
Ala Glu Arg Met Gln Asp Ile Ser Pro Glu Gln His Pro Ser Phe Asp
        35
Pro Val Lys Arg Cys Cys Gly Leu Pro Cys Asn Gly Cys Val Pro Cys
Cys Trp Pro Ser
65
       27
<210>
<211>
       16
<212>
       PRT
<213>
       Conus betulinus
<220>
<221>
       PEPTIDE
<222>
       (1)..(16)
       Xaa at residue 5, 11 and 15 is Pro or Hyp; Xaa at residue 14 is T
<223>
       rp or bromo-Trp
<400>
Cys Cys Gly Leu Xaa Cys Asn Gly Cys Val Xaa Cys Cys Xaa Xaa Ser
<210>
       28
```

<211>

```
<212>
       DNA
<213>
       Conus betulinus
<400>
caagagggat cgatagcagt tcatgatgtt taaactggga gtcttgttga ccatctatat
                                                                        60
gcttctgttt ccctttactg ctcttccgct ggatggagat caacctgcag accaacctct
                                                                       120
agagcgcatg cagtatgaca tgttacgtgc agtgaatccc tggtttgatc ccgtcaaaag
                                                                       180
gtgctgctcg aggaactgcg cagtatgcat cccttgttgc ccgaattggc cagcttgatt
                                                                       240
atcgcggcca agagtctaat gaataagtaa aacgattgca gt
                                                                       282
<210>
       29
<211>
       71
<212>
       PRT
<213>
       Conus betulinus
<400> 29
Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Tyr Met Leu Leu Phe
Pro Phe Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
Leu Glu Arg Met Gln Tyr Asp Met Leu Arg Ala Val Asn Pro Trp Phe
        35
Asp Pro Val Lys Arg Cys Cys Ser Arg Asn Cys Ala Val Cys Ile Pro
Cys Cys Pro Asn Trp Pro Ala
<210>
       30
<211>
       18
<212>
      PRT
<213>
      Conus betulinus
<220>
<221>
       PEPTIDE
<222>
       (1)..(18)
<223>
      Xaa at residue 11, 14 and 17 is Pro or Hyp; Xaa at residue 16 is
       Trp or bromo-Trp
<400> 30
Cys Cys Ser Arg Asn Cys Ala Val Cys Ile Xaa Cys Cys Xaa Asn Xaa
Xaa Ala
<210>
       31
<211>
       325
<212>
       DNA
<213>
      Conus bullatus
<400>
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                        60
gettetgttt ceeetttttg etetteegea ggatggagat caacetgeag acegacetge
                                                                       120
agagcgtatg caggacgaca tttcatctga gcagaattcc ttgcttgaga agagagttac
                                                                       180
tgacaggtgc tgcaaaggga agagggaatg cggcagatgg tgcagagatc actcgcgttg
                                                                       240
```

ttgcggtcga cgataagctg ttgatgacca gctttgttat cacggctaca tcaagtgtct 300 agtgaataag taaaatgatt gcagt 325 <210> 32 <211> 77 <212> PRT <213> Conus bullatus <400> 32 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe 10 Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro 20 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Ser Leu Leu Glu Lys Arg Val Thr Asp Arg Cys Cys Lys Gly Lys Arg Glu Cys Gly Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg 70 <210> 33 <211> 23 <212> PRT <213> Conus bullatus <220> <221> PEPTIDE <222> (1)..(23)<223> Xaa at residue 11 is Glu or gamma-carboxy Glu; Xaa at residue 15 is Trp or bromo-Trp <400> 33 Val Thr Asp Arg Cys Cys Lys Gly Lys Arg Xaa Cys Gly Arg Xaa Cys Arg Asp His Ser Arg Cys Cys 20 <210> 34 <211> 326 <212> DNA <213> Conus bullatus <400> 34 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60 gettetgttt eccetttttg etetteggea ggatggagat caacetgeag acegacetge 12.0 agagcgtatg caggatgaca tttcatctga gcagaatccc ttgcttgaga agagagttgg 180 tgacaggtgc tgcaaaggga agaggggtg cggcagatgg tgcagagatc actcacgttg 240 ttgcggtcga cgataacgtg ttgatgacca gctttgttat cacggctaca tcaagtgtct 300 tagtgattaa gtaaaacgat tgcagt 326 <210> 35 <211> 77 <212> PRT

<213> Conus bullatus

```
<400> 35
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Phe Ala Leu Arg Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Pro Leu Leu
Glu Lys Arg Val Gly Asp Arg Cys Cys Lys Gly Lys Arg Gly Cys Gly
Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
<210>
       36
<211>
       23
<212>
      PRT
<213>
      Conus bullatus
<220>
<221>
       PEPTIDE
<222>
       (1)..(23)
<223>
      Xaa at residue 15 is Trp or bromo-Trp
<400>
Val Gly Asp Arg Cys Cys Lys Gly Lys Arg Gly Cys Gly Arg Xaa Cys
Arg Asp His Ser Arg Cys Cys
       37
<210>
<211>
       331
<212>
      DNA
<213>
      Conus bullatus
<400> 37
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                       60
gettetgttt cecetttttg etetteegea ggatggagat caacetgeag acegaeetge
                                                                      120
agagcgtatg caggacgaca tttcatctga gcagaatccc ttgcttgaga agagagttgg
                                                                      180
tgaaaggtgc tgcaaaaacg ggaagagggg gtgcggcaga tggtgcagag atcactcacg
                                                                      240
ttgttgcggt cgacgataac gtgttgatga ccgaggcttt cgttatcacg gctacatcaa
                                                                      300
gtgtctagtg aataagtaaa acgattgcag t
                                                                      331
<210>
       38
<211>
       78
<212>
      PRT
<213> Conus bullatus
<400> 38
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Pro Leu Leu
                            40
```

```
Glu Lys Arg Val Gly Glu Arg Cys Cys Lys Asn Gly Lys Arg Gly Cys
Gly Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
<210>
       39
<211>
       24
<212>
       PRT
<213> Conus bullatus
<220>
<221>
      PEPTIDE
<222>
      (1)..(24)
      Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 16 i
       s Trp or bromo-Trp
<400> 39
Val Gly Xaa Arg Cys Cys Lys Asn Gly Lys Arg Gly Cys Gly Arg Xaa
Cys Arg Asp His Ser Arg Cys Cys
<210>
       40
<211>
       337
<212>
       DNA
<213>
      Conus bullatus
<400> 40
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                       60
gcttctgttt cccctttttg ctcttccgca ggacggagat caacctgcag accgacctgc
                                                                      120
agagegtatg caggaegaee ttteatetga geageateee ttgtttgaga agagaattgt
                                                                      180
tgacaggtgc tgcaacaaag ggaacgggaa gagggggtgc agcagatggt gcagagatca
                                                                      240
ctcacgttgt tgcggtcgac gatgaactgt tgatgaccga ggctttggtt atcacggcta
                                                                      300
catcaagtgt ctagtgaata agtaaaacga ttgcagt
                                                                      337
<210>
       41
<211>
       80
<212>
       PRT
<213>
      Conus bullatus
<400>
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
Ala Glu Arg Met Gln Asp Asp Leu Ser Ser Glu Gln His Pro Leu Phe
Glu Lys Arg Ile Val Asp Arg Cys Cys Asn Lys Gly Asn Gly Lys Arg
Gly Cys Ser Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
<210>
       42
```

```
<211>
       26
<212>
       PRT
<213> Conus bullatus
<220>
<221>
       PEPTIDE
<222>
       (1)..(26)
       Xaa at residue 18 is Trp or bromo-Trp
<400> 42
Ile Val Asp Arg Cys Cys Asn Lys Gly Asn Gly Lys Arg Gly Cys Ser
Arg Xaa Cys Arg Asp His Ser Arg Cys Cys
            20
<210>
       43
<211>
       337
<212>
       DNA
       Conus bullatus
<213>
<400> 43
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                       60
gettetgttt cecetttttg etetteegea ggatggagat caacetgeag accgaeetge
                                                                      120
tgagcgtatg caggacgaca tttcatctga gcggaatccc ttgtttgaga agagcgttgg
                                                                      180
tttatattgc tgccgaccca aacccaacgg gcagatgatg tgcgacagat ggtgcgaaaa
                                                                      240
aaactcacgt tgttgcggtc gacgataatg tgttgatgac cagctttgtt atcaaggcta
                                                                      300
catcaagtat ctagtgaata agtaaaacga ttgcagt
                                                                      337
<210>
       44
<211>
      77
<212>
      PRT
<213> Conus bullatus
<400> 44
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
            20
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Asn Pro Leu Phe Glu Lys
                             40
Ser Val Gly Cys Cys Arg Pro Lys Pro Asn Gly Gln Met Met Cys Asp
Arg Trp Cys Glu Lys Asn Ser Arg Cys Cys Gly Arg Arg
                    70
<210>
       45
<211>
       27
<212>
       PRT
<213> Conus bullatus
<220>
<221>
       PEPTIDE
<222>
       (1)..(27)
<223>
      Xaa at residue 21 is Glu or gamma-carboxy Glu; Xaa at residue 8 a
```

nd 10 is Pro or Hyp; Xaa at residue 19 is Trp or bromo-Trp; Xaa a

t residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulph o-Tyr or O-phospho-Tyr <400> 45 Val Gly Leu Xaa Cys Cys Arg Xaa Lys Xaa Asn Gly Gln Met Met Cys Asp Arg Xaa Cys Xaa Lys Asn Ser Arg Cys Cys <210> 46 <211> 323 DNA <212> <213> Conus bullatus <400> 46 caaqaaqqat cqataqcaqt tcatqatqtc taaactqqqa qttttqttqa ccatctqtct 60 gcttctgttt ccccttactg ctcttccgat ggatggagat caatctgtag accgacctgc 120 agaacqtatq caggacgacc tttcatctga gcagcatccc ttgtttgttc agaaaaqaaq 180 gtgttgcggc gaaggcttga catgccccag atattggaaa aacagtcaga tttgtgcttg 240 ttgttaaatg acaacgtgtc gatgaccaac ttcggtatca cgactacgcc aagtgtctaa 300 tgaataagta aaacgattgc agt 323 <210> 47 <211> 74 <212> PRT <213> Conus bullatus Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro Ala Glu Arg Met Gln Asp Asp Leu Ser Ser Glu Gln His Pro Leu Phe Val Gln Lys Arg Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr Trp Lys Asn Ser Gln Ile Cys Ala Cys Cys <210> 48 <211> 22 <212> PRT <213> Conus bullatus <220> <221> PEPTIDE <222> (1)..(22)<223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 i s Pro or Hyp; Xaa at residue 13 is Trp or bromo-Trp; Xaa at resid ue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr <400> 48

Arg Cys Cys Gly Xaa Gly Leu Thr Cys Xaa Arg Xaa Xaa Lys Asn Ser

```
Gln Ile Cys Ala Cys Cys
            20
<210>
       49
<211>
       322
<212>
      DNA
<213>
      Conus bullatus
<400> 49
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                       60
gettetgttt cecetttttg etetteegea ggatggagat caacetgeag acegaeetge
                                                                      120
tgagcgtatg caggacgaca tttcatctga gcaggatccc ttgtttgttc agaaaagaag
                                                                      180
gtgttgcggc gaaggcttga catgccccag atattggaaa aacagtcaga tttgtgcttg
                                                                      240
ttgttaaatg acaacgtgtg atgaccaact tcggtatcac gactacgcca agtgtctaat
                                                                      300
gaataagtaa aacgattgca gt
                                                                      322
       50
<210>
<211>
       74
<212>
       PRT
<213>
      Conus bullatus
<400>
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asp Pro Leu Phe
Val Gln Lys Arg Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr
Trp Lys Asn Ser Gln Ile Cys Ala Cys Cys
<210>
       51
<211>
       22
<212>
      PRT
<213> Conus bullatus
<220>
<221>
       PEPTIDE
<222>
       (1)..(22)
<223>
       Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 i
       s Pro or Hyp; Xaa at residue 13 is Trp or bromo-Trp; Xaa at resid
       ue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
       or O-phospho-Tyr
<400> 51
Arg Cys Cys Gly Xaa Gly Leu Thr Cys Xaa Arg Xaa Xaa Lys Asn Ser
Gln Ile Cys Ala Cys Cys
            20
<210>
       52
<211>
       238
```

```
<212>
       DNA
<213>
       Conus capitaneus
<400> 52
ggatccatga tgtctaaact gggagtcttg gtgaccatct gcctgcttct gtttcccctt
                                                                       60
gctgcttttc cactggatgg aaatcaacct gcagaccacc ctgcaaagcg tacgcaagat
                                                                      120
gacagttcag ctgccctgat caatacctgg attgatcatt cccattcttg ctgcagggac
                                                                      180
tgcggtgaag attgtgttgg ttgttgccgg taacgtgttg atgaccaact ttctcgag
                                                                      238
<210>
       53 ~
<211>
       70
<212>
       PRT
<213>
      Conus capitaneus
<400>
Gly Ser Met Met Ser Lys Leu Gly Val Leu Val Thr Ile Cys Leu Leu
Leu Phe Pro Leu Ala Ala Phe Pro Leu Asp Gly Asn Gln Pro Ala Asp
His Pro Ala Lys Arg Thr Gln Asp Asp Ser Ser Ala Ala Leu Ile Asn
Thr Trp Ile Asp His Ser His Ser Cys Cys Arg Asp Cys Gly Glu Asp
Cys Val Gly Cys Cys Arg
<210>
       54
<211>
       15
<212>
       PRT
<213>
      Conus capitaneus
<220>
<221>
       PEPTIDE
<222>
       (1)..(15)
      Xaa at residue 8 is Glu or gamma-carboxy Glu
<223>
<400>
Ser Cys Cys Arg Asp Cys Gly Xaa Asp Cys Val Gly Cys Cys Arg
<210>
       55
       323
<211>
<212>
       DNA
<213>
      Conus caracteristicus
<400> 55
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                       60
gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc
                                                                      120
agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata tgagaaaaag
                                                                      180
gtgttgcggc cccggcggtt catgccccgt atatttcaga gacaatttta tttgtqqttq
                                                                      240
ttgttaaatg acaacgtgtc gatgaccaac ttcattatca cgactacgcc aagtgtctaa
                                                                      300
```

323

tgaataagta aaatgattgc agt

```
<210>
       56
<211>
       74
<212>
      PRT
<213> Conus caracteristicus
<400> 56
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
            20
                                                    30
Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
Asp Met Arg Lys Arg Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys
                    70
<210>
       57
<211>
      21
<212>
      PRT
<213>
      Conus caracteristicus
<220>
<221>
      PEPTIDE
<222>
      (1)..(21)
      Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 11 is Tyr, 1
       25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400>
Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp Asn Phe
                                    10
Ile Cys Gly Cys Cys
<210>
       58
<211>
       316
<212>
      DNA
<213>
      Conus caracteristicus
<400> 58
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                       60
gcttctgttt ccccttactg ctcttccgat ggatggagat gaacctgcaa accgacctgt
                                                                      120
cgagcgtatg caggacaaca tttcatctga gcagtatccc ttgtttgaga agagacgaga
                                                                      180
ttgttgcact ccgccgaaga aatgcaaaga ccgacaatgc aaaccccaga gatgttgcgc
                                                                      240
tggacgataa cgtgttgatg accaacttta tcacggctac gtcaagtgtt tagtgaataa
                                                                      300
gtaaaatgat tgcagt
                                                                      316
<210>
       59
      75
<211>
<212>
       PRT
<213>
      Conus caracteristicus
<400> 59
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
                                    10
```

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro 25 Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg Gln Cys Lys Pro Gln Arg Cys Cys Ala Gly Arg <210> 60 <211> 22 <212> PRT <213> Conus caracteristicus <220> PEPTIDE <221> <222> (1)..(22)Xaa at residue 6, 7 and 17 is Pro or Hyp <400> 60 Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys 10 Xaa Gln Arg Cys Cys Ala <210> 61 <211> 314 <212> DNA <213> Conus caracteristicus <400> 61 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttqa ccatctqtct 60 gcttctgttt ccccttactg ctcttccact ggatggagat caacctgcag atcaatctgc 120 agagcgacct gcagagcgta cgcaggacga cattcagcag catccgttat atgatccgaa 180 aagaaggtgt tgccgttatc catgccccga cagctgccac ggatcttgct gctataagtg 240 ataacatgtt gatggccagc tttgttatca cggccacgtc aagtgtctta atgaataagt 300 aaaacgattg cagt 314 <210> 62 <211> 72 <212> PRT Conus caracteristicus <400> 62 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Ser Ala Glu Arg Pro Ala Glu Arg Thr Gln Asp Asp Ile Gln Gln His Pro

Leu Tyr Asp Pro Lys Arg Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser

50 55 60 Cys His Gly Ser Cys Cys Tyr Lys <210> 63 <211> 18 <212> PRT <213> Conus caracteristicus <220> <221> PEPTIDE <222> (1)...(18)Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 and 17 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos <400> 63 Arg Cys Cys Arg Xaa Xaa Cys Xaa Asp Ser Cys His Gly Ser Cys Cys Xaa Lys <210> 64 <211> 292 <212> DNA <213> Conus caracteristicus <400> 64 caagagggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct 60 acttetgttt tecettaetg etgtteeget ggatggagat caacatgeag accaacetge 120 acagegtetg caggacegea ttecaactga agateateee ttatttgate ecaacaaacg 180 gtgttgcccg ccggtggcat gcaacatggg atgcaagcct tgttgtggat gaccaqcttt 240 292 gttatcgcgg tcttcatgaa gtgtcttaat gaataagtaa aatgattgca gt <210> 65 <211> 69 <212> PRT <213> Conus caracteristicus <400> Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Phe Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro Ala Gln Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe Asp Pro Asn Lys Arg Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys 55 Lys Pro Cys Cys Gly <210> 66 <211> 15 <212> PRT

<213> Conus caracteristicus

```
<220>
<221>
       PEPTIDE
<222>
       (1)..(15)
<223>
       Xaa at residue 3, 4 and 13 is Pro or Hyp
<400>
Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Lys Xaa Cys Cys
       67
<210>
<211>
       293
<212>
       DNA
<213>
       Conus caracteristicus
<400>
       67
caagagggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct
                                                                           60
acttetgttt teectaactg etgtteeget ggatggagat caacatgeag accaacetge
                                                                          120
agagegtetg catgacegee ttecaactga aaatcateee ttatatgate eegteaaacq
                                                                          180
gtgttgcgat gattcggaat gcgactattc ttgctggcct tgctgtatgt ttggataacc
                                                                          240
tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt
                                                                          293
<210>
       68
<211>
       71
<212>
       PRT
<213>
       Conus caracteristicus
<400> 68
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Phe
Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
Trp Pro Cys Cys Met Phe Gly
                     70
<210>
       69
<211>
       17
<212>
       PRT
<213>
       Conus caracteristicus
<220>
<221>
       PEPTIDE
<222>
       (1)..(17)
       Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 i
<223>
       s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o
       r O-phospho-Tyr
<400>
       69
Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Met
```

Phe

```
<210>
       70
<211>
       232
<212>
       DNA
<213>
       Conus caracteristicus
<400> 70
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt
                                                                        60
actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg taagcaggac
                                                                       120
gtttcatctg aacagcatcc cttctttgat cccgtcaaac ggtgttgccg ccggtgttac
                                                                       180
atgggatgca tecettgttg ettttaaegt gttgatgace aacttteteg ag
                                                                       232
<210>
       71
<211>
       68
<212>
       PRT
<213>
       Conus caracteristicus
<400> 71
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
Arg Pro Ala Glu Arg Lys Gln Asp Val Ser Ser Glu Gln His Pro Phe
        35
Phe Asp Pro Val Lys Arg Cys Cys Arg Arg Cys Tyr Met Gly Cys Ile
Pro Cys Cys Phe
<210>
       72
<211>
       14
<212>
      PRT
<213>
      Conus caracteristicus
<220>
<221>
       PEPTIDE
<222>
       (1)...(14)
       Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Ty
<223>
       r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400>
Cys Cys Arg Arg Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
<210>
       73
<211>
       323
<212>
       DNA
<213>
       Conus circumcisus
<400> 73
caagaaggat cgatagcagt tcatgatgtc taaactgggg gtattgttga ccatctqtct
                                                                        60
gettetgttt cecettactg etettecaat ggatggagat caacetgeag accaacetge
                                                                       120
agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata agagacgaaa
                                                                       180
gtgttgcggc aaagacgggc catgccccaa atatttcaaa gacaatttta tttgtggttg
                                                                       240
ttgttaaatg acaacgtgtc gatgaccaac ttcgttatca cgattcgcca agtgtcttaa
                                                                       300
```

```
tgaataagta aaatgattgc agt
                                                                      323
<210>
       74
<211>
       74
<212>
       PRT
<213>
       Conus circumcisus
<400> 74
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
Asp Lys Arg Arg Lys Cys Cys Gly Lys Asp Gly Pro Cys Pro Lys Tyr
Phe Lys Asp Asn Phe Ile Cys Gly Cys Cys
<210>
       75
<211>
       23
<212>
      PRT
<213> Conus circumcisus
<220>
<221> PEPTIDE
<222>
      (1)..(23)
      Xaa at residue 9 and 11 is Pro or Hyp; Xaa at residue 13 is Tyr,
       125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T
<400> 75
Arg Lys Cys Cys Gly Lys Asp Gly Xaa Cys Xaa Lys Xaa Phe Lys Asp
Asn Phe Ile Cys Gly Cys Cys
<210>
       76
<211>
       293
<212>
       DNA ·
<213>
      Conus dalli
<400> 76
caagagggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct
                                                                       60
acttctgttt tccctaactg ctgttccgct ggatggagat caacatgcag accaacctgc
                                                                      120
agagegtetg caggacegee ttecaactga aaatcateee ttatatgate eegteaaacg
                                                                      180
gtgttgcgat gattcggaat gcgactattc ttgctggcct tgctgtattt tatcataacc
                                                                      240
tttgttatcg cggcctcatc aagtgtcaaa tgaataagta aaatgattgc agt
                                                                      293
<210>
       77
<211>
       71
<212>
       PRT
<213>
      Conus dalli
<400> 77
```

Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Phe Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys 55 Trp Pro Cys Cys Ile Leu Ser <210> 78 <211> 18 <212> PRT <213> Conus dalli <220> <221> PEPTIDE <222> <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 i s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at resid ue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o r O-phospho-Tyr <400> 78 Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile Leu Ser <210> 79 <211> 299 <212> DNA <213> Conus dalli <400> 79 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatttgtct 60 acttctgttt ccccttactg ctgttccact ggatggagat cagcctgcag accgacctgc 120 agagogtatg caggacggca tttcatctga acatcatcca ttttttgatt ccqtcaaaaa 180 gaaacaacag tgttgcccgc cggtggcatg caacatggga tgcgagcctt gttgtggatg 240 accagetttg ttategegge teatgaagtg teetaatgaa taagtaaaac gattgeagt 299 <210> 80 72 <211> <212> PRT <213> Conus dalli <400> 80 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro 20 Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu His His Pro Phe Phe

```
Asp Ser Val Lys Lys Gln Gln Cys Cys Pro Pro Val Ala Cys Asn
Met Gly Cys Glu Pro Cys Cys Gly
<210>
      81
<211>
       17
<212>
       PRT
<213> Conus dalli
<220>
<221>
      PEPTIDE
<222>
      (1)..(17)
      Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 14 is Glu or
       gamma-carboxy Glu; Xaa at residue 5, 6 and 15is Pro or Hyp
<400> 81
Xaa Gln Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Xaa Xaa Cys
Cys
<210>
       82
       290
<211>
<212>
       DNA
<213>
     Conus dalli
<400> 82
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga tcatatgtct
                                                                       60
atttctgttt ccccttactg ctgttcagct caatggagat cagcctgcag accaatctgc
                                                                      120
agagegtatg caggacaaaa tttcatctga acatcatccc ttttttgatc ccgtcaaacq
                                                                      180
ttgttgcaac geggggtttt geegettegg atgeaegeet tgttgttggt gaeeagettt
                                                                      240
gttatcgcgg cctcatcaag tgtctaatga ataagtaaaa tgattgcagt
                                                                      290
<210> 83
<211>
      69
<212>
      PRT
<213> Conus dalli
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Phe Leu Phe
Pro Leu Thr Ala Val Gln Leu Asn Gly Asp Gln Pro Ala Asp Gln Ser
Ala Glu Arg Met Gln Asp Lys Ile Ser Ser Glu His His Pro Phe Phe
Asp Pro Val Lys Arg Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys
    50
                        55
Thr Pro Cys Cys Trp
65
<210>
       84
<211>
       16
<212>
       PRT
<213> Conus dalli
```

```
<220>
<221>
      PEPTIDE
<222>
      (1)..(16)
     Xaa at residue 13 is Pro or Hyp; Xaa at residue 16 is Trp or brom
       o-Trp
<400> 84
Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys Thr Xaa Cys Cys Xaa
                                    10
<210>
      85
<211>
      288
<212>
     DNA
<213> Conus distans
<400> 85
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccatctttct
                                                                       60
gcttctgttt ccccttactg ctgttccgct ggatggagat caacccgcag acggacttgc
                                                                      120
agagcqcatq caggacqaca qttcagctqc actqattaga qactqqcttc ttcaaacccq
                                                                      180
acagtgttgt gtgcatccat gcccatgcac gccttgctgt agatgaccag ctttgtcatc
                                                                      240
gcggctacgt caagtatcta atgaataagt aagtaaaacg attgcagt
                                                                      288
<210> 86
<211>
      67
<212>
      PRT
<213> Conus distans
<400> 86
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Phe Leu Leu Phe
Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gly Leu
Ala Glu Arg Met Gln Asp Asp Ser Ser Ala Ala Leu Ile Arg Asp Trp
Leu Leu Gln Thr Arg Gln Cys Cys Val His Pro Cys Pro Cys Thr Pro
    50
                        55
                                            60
Cys Cys Arg
<210>
       87
<211>
       14
<212>
       PRT
<213>
      Conus distans
<220>
<221>
       PEPTIDE
<222>
      (1)..(14)
<223>
      Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 11 i
       s Pro or Hyp
<400> 87
Xaa Cys Cys Val His Xaa Cys Xaa Cys Thr Xaa Cys Cys Arg
                5
<210>
       88
<211>
       303
<212>
       DNA
<213> Conus ermineus
```

```
<400> 88
acctcaagag ggatcgatcg cagttcatga tgtctaaact gggagccttg ttgaccatct
                                                                       60
gtctgcttct gtttcccatt actgctcttc tgatggatgg agatcagcct gcagaccgac
                                                                      120
ctgcagagcg tacggaggat gacatttcat ctgactacat tccctqttqc aqttqqccat
                                                                      180
gcccccgata ctccaacggt aaacttgttt gtttttgttg ccttggatga taatgtgttg
                                                                      240
atgaccaact ttgttatcac ggctacgtca agtgtctact gaataagtaa aatgattgca
                                                                      300
gta
                                                                      303
<210>
       89
<211>
       67
<212>
       PRT
<213>
      Conus ermineus
<400> 89
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Phe
Pro Ile Thr Ala Leu Leu Met Asp Gly Asp Gln Pro Ala Asp Arg Pro
Ala Glu Arg Thr Glu Asp Asp Ile Ser Ser Asp Tyr Ile Pro Cys Cys
Ser Trp Pro Cys Pro Arg Tyr Ser Asn Gly Lys Leu Val Cys Phe Cys
Cys Leu Gly
<210>
       90
<211>
       20
<212>
       PRT
<213>
       Conus ermineus
<220>
<221>
       PEPTIDE
<222>
       (1)..(20)
      Xaa at residue 5 and 7 is Pro or Hyp; Xaa at residue4 is Trp or
<223>
       bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-i
       odo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400> 90
Cys Cys Ser Xaa Xaa Cys Xaa Arg Xaa Ser Asn Gly Lys Leu Val Cys
Phe Cys Cys Leu
<210>
       91
<211>
       241
<212>
       DNA
<213>
      Conus generalis
<400>
       91
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctqgttct gtttcccctt
                                                                       60
actgctcttc cactggatgg agaacaacct gtagaccgac atgccgagca tatgcaggat
                                                                      120
```

gacaattcag ctgcacagaa cccctgggtt attgccatca gacagtgttg cacgttctqc

```
aactttggat gccaaccttg ttgcctcacc tgataacgtg ttgatgacca actttctcga
                                                                      240
                                                                       241
<210>
       92
<211>
       70
<212>
       PRT
<213>
       Conus generalis
<400> 92
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val
                                     10
Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp
Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro
Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys
Gln Pro Cys Cys Leu Thr
<210>
       93
<211>
       16
<212>
      PRT
<213> Conus generalis
<220>
<221>
      PEPTIDE
<222>
       (1)...(16)
<223>
       Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 is Pro or
       Нур
<400> 93
Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Leu Thr
<210>
       94
<211>
       241
<212>
      DNA
<213>
     Conus generalis
<400> 94
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctggttct gtttcccctt `
                                                                        60
actgetette cactggatgg agaacaacet gtagacegae atgeegagea tatgeaggat
                                                                       120
gacaattcag ctgcacagaa cccctgggtt attgccatca gacagtgttg cacgttctqc
                                                                       180
aactttggat gccagccttg ttgcgtcccc tgataacgtg ttgatgacca actttctcga
                                                                       240
g
                                                                       241
<210>
       95
<211>
       70
<212>
       PRT
<213>
      Conus generalis
<400> 95
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val
```

```
Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp
Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro
Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys
Gln Pro Cys Cys Val Pro
<210>
       96
<211>
       16
<212>
      PRT
<213> Conus generalis
<220>
<221>
       PEPTIDE
<222>
       (1)..(16)
       Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 and 16 is
       Pro or Hyp
<400> 96
Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Val Xaa
<210>
       97
<211>
       862
<212>
       DNA
<213> Conus geographus
<400>
gtcgactcta gaggatccga caacaaagag tcaaccccac tgccacgtca agaqcqaaqc
                                                                       60
gccacagcta agacaagagg gatcgatagc agttcatgat gtctaaactg ggagtcttgt
                                                                      120
tgaccatctg tctgcttctg tttcccctta ctgctcttcc gatggatgga gatgaacctg
                                                                      180
caaaccgacc tgtcgagcgt atgcaggaca acatttcatc tgagcagtat cccttqtttq
                                                                      240 .
agaagagacg agattgttgc actccgccga agaaatgcaa agaccgacaa tgcaaacccc
                                                                      300
agagatgttg cgctggacga taacgtgttg atgaccaact ttatcacggc tacgtcaagt
                                                                      360
gtttagtgaa taagtaaaat gattgcagtc ttgctcagat ttgcttttgt gttttggtct
                                                                      420
aaagatcaat gaccaaaccg ttgttttgat gcggattgtc atatatttct cgattccaat
                                                                      480
ccaacactag atgatttaat cacgatagat taattttcta tcaatgcctt gatttttcgt
                                                                      540
ctgtcatatc agttttgttt atatttattt tttcgtcact gtctacacaa acgcatgcat
                                                                      600
geacgeatge acgeacaeae geacgeacge tegeacaaae atgegegege acgeacaeae
                                                                      660
acacacaca acacaaacac acacacaagc aatcacacaa ttattgacat tatttattta
                                                                      720
ttcattgatg tatttgttat tcgtttgctt gtttttagaa tagtttgagg ccgtcttttt
                                                                      780
ggatttattt gaactgcttt attgtatacg agtacttcgt gctttgaaac actgctgaaa
                                                                      840
ataaaacaaa cactgacgta gc
                                                                      862
```

```
<211>
       75
<212>
       PRT
<213>
       Conus geographus
<400>
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe
Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg
Gln Cys Lys Pro Gln Arg Cys Cys Ala Gly Arg
<210>
       99
<211>
       22
<212>
       PRT
       Conus geographus
<220>
<221>
       PEPTIDE
<222>
       (1)..(22)
<223>
      Xaa at residue 6, 7 and 17 is Pro or Hyp
<400>
Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys
Xaa Gln Arg Cys Cys Ala
<210>
       100
<211>
       860
<212>
       DNA
<213>
       Conus geographus
<400> 100
ggccagacga caacaaagag tcaaccccac tgccacgtca agagcgaagc gccacagcta
                                                                       60
agacaagagg gatcgatagc agttcatgat gtctaaactg ggagtcttgt tgaccatctg
                                                                      120
tetgettetg ttteeeetta etgetettee gatggatgga gatgaacetg caaacegace
                                                                      180
tgtcgagcgt atgcaggaca acatttcatc tgagcagtat cccttgtttg agaagagacg
                                                                      240
agattgttgc actccgccga ggaaatgcaa agaccgacga tgcaaaccca tgaaatgttg
                                                                      300
cgctggacga taacgtgttg atgaccaact ttatcacggc tagctcagtg tttagtgaat
                                                                      360
aagtaaaatg attgcagtct tgctcagatt gcttttgtgt ttttggtctaa gatcaatgac
                                                                      420
caaaccgttg ttttgatgcg gattgtcata tatttctcga ttccaatcca acactagatg
                                                                      480
atttaatcac gatagattaa ttttctatca atgccttgat ttttcgtctg tcatatcagt
                                                                      540
tttgtttata tttattttt cgtcactgtc tacacaaacg catgcatgca cgcatgcacg
                                                                      600
cacacacgca cgcacgctcg cacaaacatg cgcgcgcacg cacacacaca cacacacaca
                                                                      660
```

```
aacacacaca cgaagcaatc acacaattag ttgacattat ttatttattc attgatgtat
                                                                       720
ttgttattcg tttgcttgtt tttagaatag tttgaggccg tctttttgga tttatttgaa
                                                                       780
ctgctttatt gtatacgagt acttcgtgct ttgaaacact gctgaaaata aaacaaacac
                                                                       840
tgacgtagca aaaaaaaaa
                                                                       860
<210>
       101
<211>
       75
<212>
       PRT
<213> Conus geographus
<400> 101
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe
Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg 50 55 60
Arg Cys Lys Pro Met Lys Cys Cys Ala Gly Arg 65 70 75
<210> 102
<211> 22
<212> PRT
<213> Conus geographus
<220>
<221> PEPTIDE
<222>
       (1)..(22)
       Xaa at residue 6, 7 and 17 is Pro or Hyp
<223>
Arg Asp Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Arg Cys Lys
Xaa Met Lys Cys Cys Ala
            20
<210>
      103
<211> 22
<212> PRT
<213> Conus geographus
<220>
<221>
       PEPTIDE
<222>
       (1)..(22)
       Xaa at residue 6, 7 and 17 is Pro or Hyp
<400> 103
Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Arg Cys Lys
Xaa Leu Lys Cys Cys Ala
<210>
       104
<211>
       321
```

<212>

DNA

```
<213> Conus gloriamaris
<400>
       104
ctcactatag gaattcgagc tcggtacacg ggatcgatag cagttcatga tgtctaaact
                                                                       60
gggagcettg ttgaccatct gtctacttct gttttcccta actgctgttc cgctggatgg
                                                                      120
agatcaacat gcagaccaac ctgcagagcg tctgcatgac cgccttccaa ctgaaaatca
                                                                      180
tecettatat gateeegtea aacggtgttg egatgatteg gaatgegaet attettgetg
                                                                      240
gccttgctgt atgtttggat aacctttgtt atcgcggcct cgataagtgt ctaatgaata
                                                                      300
agtaaaacga ttgcagtagg c
                                                                      321
<210>
       105
<211>
       71
<212>
       PRT
<213>
      Conus gloriamaris
<400> 105
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Phe
Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
Trp Pro Cys Cys Met Phe Gly
<210>
       106
       17
<211>
<212>
      PRT
<213> Conus gloriamaris
<220>
       PEPTIDE
<221>
<222>
       (1)..(17)
      Xaa at residue is 6 Glu or gamma-carboxy Glu; Xaa at residue 13 i
       s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at resid
       ue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o
       r O-phospho-Tyr
<400> 106
Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Met
                                    10
Phe
<210>
       107
<211>
       257
<212>
       DNA
<213>
      Conus gloriamaris
<400> 107
gttcatgatg tctaaactgg gagtcttgtt gatcatctgt ctacttctgt ttccccttac
                                                                       60
tgctgttccg ctggatggag atcaacctgc agaccgatat gcagagcgta tgcaggacga
                                                                      120
```

```
catttcatct gaacatcatc ccatgtttga tgccgtcaga gggtgttgcc atctgttggc
                                                                      180
atgccgcttc ggatgctcgc cttgttgttg gtgatcagct ttgttatcgc ggcctcatca
                                                                      240
agtgactcta atgcaaa
                                                                      257
<210>
       108
<211>
       69
<212>
       PRT
<213>
       Conus gloriamaris
<400> 108
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Phe
Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Tyr
            20
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His His Pro Met Phe
Asp Ala Val Arg Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys
Ser Pro Cys Cys Trp
<210>
       109
<211>
       17
<212>
       PRT
<213>
       Conus gloriamaris
<220>
<221>
       PEPTIDE
<222>
       (1)..(17)
       Xaa at residue 14 is Pro or Hyp; Xaa at residue 17 is Trp or brom
<223>
       o-Trp
<400> 109
Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Xaa Cys Cys
Xaa
<210>
       110
<211>
       471
<212>
       DNA
<213>
      Conus gloriamaris
<400> 110
gagacgacaa ggaacagtca accccacagc cacgccaaga gcagacagcc acagctacgt
                                                                       60
gaagaagggt ggagagaggt tcgtgatgtt gaaaatggga gtggtgctat tcatcttcct
                                                                      120
ggtactgttt cccctggcaa cgctccagct ggatgcagat caacctgtag aacgatatgc
                                                                      180
ggagaacaaa cagctcctca acccagatga aaggagggaa atcatattgc atgctctggg
                                                                      240
gacgcgatgc tgttcttggg atgtgtgcga ccacccgagt tgtacttgct gcggcggtta
                                                                      300
gcgccgaaca tccatggcgc tgtgctgggc ggttttatcc aacaacgaca gcgtttgttg
                                                                      360
atttcatgta tcattgcgcc cacgtctctt gtctaagaat gacgaacatg attgcactct
                                                                      420
ggttcagatt tcgtgttctt ttctgacaat aaatgacaaa actccaaaaa a
                                                                      471
```

```
<210>
      111
<211>
      71
<212>
      PRT
<213>
      Conus gloriamaris
<400> 111
Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe Pro
Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr Ala
Glu Asn Lys Gln Leu Leu Asn Pro Asp Glu Arg Arg Glu Ile Ile Leu
His Ala Leu Gly Thr Arg Cys Cys Ser Trp Asp Val Cys Asp His Pro
Ser Cys Thr Cys Cys Gly Gly
<210> 112
<211>
      16
<212> PRT
<213> Conus gloriamaris
<220>
<221>
     PEPTIDE
      (1)..(16)
<223> Xaa at residue 10 is Pro or Hyp; Xaa at residue 4 is Trp or bromo '
      -Trp
<400> 112
Cys Cys Ser Xaa Asp Val Cys Asp His Xaa Ser Cys Thr Cys Cys Gly
<210> 113
<211>
      304
<212>
      DNA
<213>
      Conus laterculatus
<400> 113
cgacctcaag aaggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgaccat
                                                                      60
ctgtctgctt ctgtttcccc ttactgctct tccgatggat ggagatcaac ctgcagaccg
                                                                     120
acctgcagag cgtatgcagg acgtttcatc tgaacagcat cccttgtatg atcccgtcaa
                                                                     180
acggtgttgc gactggccat gcagcggatg catcccttgt tgctaatagt aacaacqtgt
                                                                     240
tgataaccaa ctttcttacc acgactacgt caagtgtcta atgaataagt aaaatgattg
                                                                     300
cagt
                                                                     304
<210>
      114
<211>
       65
<212>
       PRT
<213> Conus laterculatus
<400> 114
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
```

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Pro

20 25 30 Ala Glu Arg Met Gln Asp Val Ser Ser Glu Gln His Pro Leu Tyr Asp 40 Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ser Gly Cys Ile Pro Cys Cys <210> 115 <211> 13 <212> PRT <213> Conus laterculatus <220> <221> PEPTIDE <222> (1)..(13)<223> Xaa at residue 5 and 11 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Trp <400> 115 Cys Cys Asp Xaa Xaa Cys Ser Gly Cys Ile Xaa Cys Cys <210> 116 313 <211> <212> DNA <213> Conus laterculatus <400> 116 cgacctcaag aaggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgaccat 60 ctgtctgctt ctgtttcccc ttactgctct ggatggagat caacctgcag accqacttqc 120 agagcgtatg caggacgaca tttcatctga gcagcatccc tttgaaaaga gacgagactg 180 ttgcacacct ccgaagaaat gcagagaccg acaatgcaaa cctgcacgtt gttgcgqaqq 240 ataacgtgtt gatgaccaac tttgttatca cggctacgtc aagtgtctag tgaataagta 300 aaacgattgc agt 313 <210> 117 <211> 71 <212> PRT <213> Conus laterculatus <400> 117 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe 10 Pro Leu Thr Ala Leu Asp Gly Asp Gln Pro Ala Asp Arg Leu Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Phe Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Arg Asp Arg Gln Cys Lys Pro Ala Arg Cys Cys Gly Gly

```
<210>
      118
<211>
      22
<212>
      PRT
<213> Conus laterculatus
<220>
<221>
      PEPTIDE
<222>
      (1)..(22)
<223>
      Xaa at residue 6, 17 and 17 is Pro or Hyp
<400> 118
Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Arg Asp Arg Gln Cys Lys
                                    10
Xaa Ala Arg Cys Cys Gly
            20
<210>
       119
<211>
       314
<212>
      DNA
<213> Conus laterculatus
<400> 119
gggatcgata gcagttcatg atgtctaaac tgggagtctt gttgaccatc tgtctgcttc
                                                                       60
tgtttcccct tactgctctt ccgatggatg gagatcaact tgcacgccga tctgcagagc
                                                                      120
gtatgcagga caacatttca tctgagcagc atcacctctt tgaaaaggaga cgaccaccat
                                                                      180
gttgcaccta tgacgggagt tgcctaaaag aatcatgcat gcgtaaagct tgttgcggat
                                                                      240
gataacgtgt tgatgaccaa ctttgttatc acggctactc aagtgtctaa tgaataagta
                                                                      300
aaatgattgc agta
                                                                      314
      120
<210>
<211>
      74
<212>
      PRT
<213>
      Conus laterculatus
<400> 120
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Arg Arg Ser
Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His His Leu Phe
Glu Lys Arg Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys
Glu Ser Cys Met Arg Lys Ala Cys Cys Gly
<210>
      121
<211>
       22
<212> PRT
<213> Conus laterculatus
<220>
<221>
      PEPTIDE
<222>
       (1)..(22)
      Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 2 a
<223>
```

nd 3 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-

Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr <400> 121 Arg Xaa Xaa Cys Cys Thr Xaa Asp Gly Ser Cys Leu Lys Xaa Ser Cys Met Arg Lys Ala Cys Cys <210> 122 <211> 314 <212> DNA <213> Conus laterculatus <400> 122 gggatcgata gcagttcatg atgtctaaac tgggagtctt gttgaccacc tgtctgcttc 60 tgtttcccct tactgctctt ccgatggatg gagatcaact tgcacgccga cctgcagagc 120 gtatgcagga caacatttca tctgagcagc atcccttctt tgaaaggaga cgaccaccat 180 gttgcaccta tgacgggagt tgcctaaaag aatcatgcaa gcgtaaagct tgttgcggat 240 aataacgtgt tgatgaccaa ctttgttatc acggctactc aagtgtctaa tgaataagta 300 aaatgattgc agta 314 <210> 123 <211> 74 <212> PRT <213> Conus laterculatus <400> 123 Met Met Ser Lys Leu Gly Val Leu Leu Thr Thr Cys Leu Leu Phe 10 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Arg Arg Pro Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe Glu Arg Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys Glu Ser Cys Lys Arg Lys Ala Cys Cys Gly <210> 124 <211> 22 <212> PRT <213> Conus laterculatus <220> <221> PEPTIDE <222> (1)..(22)Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 2 a <223> nd 3 is Pro or Hyp; Xaa at residue7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr <400> Arg Xaa Xaa Cys Cys Thr Xaa Asp Gly Ser Cys Leu Lys Xaa Ser Cys

Lys Arg Lys Ala Cys Cys

```
<210>
       125
<211>
       247
<212>
       DNA
<213>
       Conus leopardus
<400> 125
ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttcccctt
                                                                        60
actgctcttc ggctggttgg agatcaacct gcagagcgac ctgcaaagcg tacgcaggac
                                                                       120
gacattccag atggacagca tccgttaaat gataggcaga taaactgttg cccgtggcca
                                                                       180
tgccctagta catgccgcca tcaatgctgc cattaatgat aacgtgttga tgaccaactt
                                                                       240
tctcgag
                                                                       247
<210>
       126
<211>
       71
<212>
       PRT
<213>
       Conus leopardus
<400> 126
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu
                                     10
                                                         15
Leu Phe Pro Leu Thr Ala Leu Arg Leu Val Gly Asp Gln Pro Ala Glu
Arg Pro Ala Lys Arg Thr Gln Asp Asp Ile Pro Asp Gly Gln His Pro
Leu Asn Asp Arg Gln Ile Asn Cys Cys Pro Trp Pro Cys Pro Ser Thr
Cys Arg His Gln Cys Cys His
<210>
       127
<211>
       19
<212>
       PRT
<213> Conus leopardus
<220>
       PEPTIDE
<221>
<222>
       (1)..(19)
       Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 10 i
       s Pro or Hyp; Xaa at residue 7 is Trp or bromo-Trp
<400>
Xaa Ile Asn Cys Cys Xaa Xaa Xaa Cys Xaa Ser Thr Cys Arg His Gln
Cys Cys His
<210>
       128
<211>
       244
<212>
       DNA
<213>
       Conus lividus
<400>
       128
ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttcccctt
                                                                        60
actgctcttc ggctggttag agatcaacct gcagagcgac ctgcaaagcg tacgcaggac
                                                                       120
```

```
gacattccaa atggacagga tccgttaatt gataggcaga taaattgttg cccttggcca
                                                                       180
tgccctgatt catgccacta tcaatgctgc cactgataac gtgttgatga ccaactttct
                                                                       240
cgag
                                                                       244
<210>
       129
<211>
       71
<212>
       PRT
       Conus lividus
<213>
<400> 129
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu
Leu Phe Pro Leu Thr Ala Leu Arg Leu Val Arg Asp Gln Pro Ala Glu
Arg Pro Ala Lys Arg Thr Gln Asp Asp Ile Pro Asn Gly Gln Asp Pro
Leu Ile Asp Arg Gln Ile Asn Cys Cys Pro Trp Pro Cys Pro Asp Ser
Cys His Tyr Gln Cys Cys His
<210>
       130
<211>
       19
<212>
      PRT
<213> Conus lividus
<220>
<221>
       PEPTIDE
<222>
       (1)..(19)
       Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 10 i
<223>
       s Pro or Hyp; Xaa at residue 7 is Trp or bromo-Trp; Xaa at residu
       e 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o
       r O-phospho-Tyr
<400> 130
Xaa Ile Asn Cys Cys Xaa Xaa Xaa Cys Xaa Asp Ser Cys His Xaa Gln
                                     10
Cys Cys His
<210>
       131
<211>
       275
<212>
       DNA
<213>
       Conus lynceus
<400>
aaggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgaccat ctgtctgctt
                                                                        60
ctgtttcccc ttactgctct tccgatggat ggagatcaat ctgcagaccg acttgcagag
                                                                       120
cgtatgcagg acaacatttc atctgagcag catcccttct ttgaaaagag aggacgagac
                                                                       180
tgttgcacac ctccgaggaa atgcagagac cgagcctgca aacctcaacg ttgttqcqqa
                                                                       240
ggataagctg ttgatgacca actttgttat acggc
                                                                       275
<210>
       132
```

<211>

```
<212>
       PRT
<213>
       Conus lynceus
<400> 132
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Ala Asp Arg Leu
Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
Glu Lys Arg Gly Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Arg Asp
Arg Ala Cys Lys Pro Gln Arg Cys Cys Gly Gly
<210>
       133
<211>
       23
<212>
       PRT
<213>
       Conus lynceus
<220>
<221>
       PEPTIDE
<222>
       (1)..(23)
      Xaa at residue 7, 8 and 18 is Pro or Hyp
<223>
<400>
Gly Arg Asp Cys Cys Thr Xaa Xaa Arg Lys Cys Arg Asp Arg Ala Cys
Lys Xaa Gln Arg Cys Cys Gly
            20
<210>
       134
<211>
       803
<212>
       DNA
<213>
       Conus magus
<400> 134
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                       60
gcttctgttt ccccttactg ctcttccgat ggatggagat gaacctgcaa accqacctgt
                                                                      120
cgagcgtatg caggacaaca tttcatctga gcagtatccc ttgtttgaga agagacgaga
                                                                      180
ttgttgcact ccgccgaaga aatgcaaaga ccgacaatgc aaaccccaga gatgttgcqc
                                                                      240
tggacgataa cgtgttgatg accaacttta tcacggctac gtcaagtgtt tagtgaataa
                                                                      300
gtaaaatgat tgcagtcttg ctcagatttg cttttgtgtt ttggtctaaa gatcaatgac
                                                                      360
caaaccgttg ttttgatgcg gattgtcata tatttctcga ttccaatcca acactagatg
                                                                      420
atttaatcac gatagattaa ttttctatca atgccttgat ttttcgtctg tcatatcagt
                                                                      480
tttgtttata tttattttt cgtcactgtc tacacaaacg catgcatgca cgcatgcacg
                                                                      540
cacacacgca cgcacgctcg cacaaacatg cgcgcgcacg cacacacaca cacacacac
                                                                      600
caaacacaca cacgaagcaa tcacacaatt agttgacatt atttatttat tcattgatgt
                                                                      660
atttgttatt cgtttgcttg tttttagaat agtttgaggc cgtctttttg gatttatttg
                                                                      720
```

aactgcttta ttgtatacga gtacttcgtg cggggaaaca ctgctgaaaa taaaacaaac	780
actgacgtag caaaaaaaa aaa	803
<210> 135 <211> 75 <212> PRT <213> Conus magus	
<400> 135	
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe 1 5 10 15	
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro 20 25 30	
Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe 35 40 45	
Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg 50 55 60	
Gln Cys Lys Pro Gln Arg Cys Cys Ala Gly Arg 65 70 75	
<210> 136 <211> 22 <212> PRT <213> Conus magus	
<220> <221> PEPTIDE <222> (1)(22) <223> Xaa at residue 6 and 7 is Pro or Hyp	
<400> 136 Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys 1 5 10 15	
Xaa Gln Arg Cys Cys Ala 20	
<210> 137 <211> 656 <212> DNA <213> Conus magus	
<400> 137 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct	60
gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc	120
agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata tgagaaaaag	180
gtgttgcggc cccggcggtt catgccccgt atatttcaga gacaatttta tttgtggttg	240
ttgttaaatg acaacgtgtc gatgaccaac ttcattatca cgactacgcc aagtgtctaa	300
tgaataaata aaatgattgc agtctcgctc agatttgctt ttgtattttg gtctaaagat	360
caatgaccaa accgttgttt tggtgtggat tttcatatat ttctcgagtc ctatccaaca	420
ctagatgatt taatcacgat agatctgatt tttttatcaa aggcttggtt tttcgtctgt	480

```
cacatcagtt ttgtttatat ttaatttttc gtcactgatt acacacacgc atgaacgcac
                                                                    540
600
cacacacaca cacgegegeg egeggegeca tetagtageg eegegaegae acacac
                                                                    656
<210>
       138
<211>
       74
<212>
       PRT
<213>
       Conus magus
<400> 138
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
            20
Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
Asp Met Arg Lys Arg Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr 50 55 60
Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys
<210>
       139
<211>
       21
       PRT
<212>
<213> Conus magus
<220>
<221>
       PEPTIDE
<222>
       (1)..(21)
<223>
       Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue is 11 Tyr, 1
       25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
, <400> 139
Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp Asn Phe
                                    10
Ile Cys Gly Cys Cys
<210>
       140
<211>
       594
<212>
       DNA
<213>
       Conus magus
<400> 140
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgttt
                                                                     60
gcttctgttt ccccttactg ctcttccgag ggatggagat caatctgtag accgacctgc
                                                                    120
agagcgtatg caggacgaca tttcatctga gctgcatccc ttgtcaatca gaaaaagaat
                                                                    180
gtgttgcggc gagagtgcgc catgccccag ctatttcaga aacagtcaga tttgtcattg
                                                                    240
ttgttaaatg acaacgtgtc gatgaccacc ttcgttatca cgactaatga taagtaaaat
                                                                    300
gattgcagtc tcgctcagat ttgcttttgt attttggtct aaagatcaat gaccaaaccg
                                                                    360
ttgttttgat gtggattttc atatatttct cgagtcctat ccaacactag atgatttaat
                                                                    420
```

```
cacgatagat ctgatttttt tatcaaagcc ttggtttttc gtctgtcaca tcagttttgt
                                                                   480
ttatatttaa tttttcgtca ctgattacac acacgcatga acgcacagac gtactaacac
                                                                   540
594
<210>
      141
<211>
      74
<212>
      PRT
<213>
      Conus magus
<400> 141
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Arg Asp Gly Asp Gln Ser Val Asp Arg Pro
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Leu His Pro Leu Ser
Ile Arg Lys Arg Met Cys Cys Gly Glu Ser Ala Pro Cys Pro Ser Tyr
Phe Arg Asn Ser Gln Ile Cys His Cys Cys
<210>
      142
<211>
      22
<212>
      PRT
<213> Conus magus
<220>
<221>
      PEPTIDE
<222>
       (1)..(22)
      Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 8 an
<223>
      d 10 is Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo
      -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400> 142
Met Cys Cys Gly Xaa Ser Ala Xaa Cys Xaa Ser Xaa Phe Arg Asn Ser
Gln Ile Cys His Cys Cys
           20
<210>
      143
<211>
      501
<212>
      DNA
<213>
      Conus magus
<400> 143
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctqtct
                                                                    60
gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc
                                                                   120
agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata agagacaaaa
                                                                   180
gtgttgcggc cccggcggtt catgccccgt atatttcaca gacaatttta tttgtgqttq
                                                                   240
ttgttaaatg acaacgtgtc gatgaccaac ttcattatca cgactacgcc aagtgtctaa
                                                                   300
```

tgaataaata aaatgattgc agtctcgctc agatttgctt ttgtatttgg tctaaagatc

```
aatgaccaaa ccgttgtttt ggtgctggat tttcatatat ttctcgattc ctatccaaca
                                                                      420
ctagatgatt taatcacgat agatctgatt tttttatcaa tgccttaatt ttttgctctg
                                                                      480
tcatatcagt tttgtttata t
                                                                      501
<210>
       144
<211>
       74
<212>
       PRT
<213>
      Conus magus
<400> 144
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
            20
Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
Asp Lys Arg Gln Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
Phe Thr Asp Asn Phe Ile Cys Gly Cys Cys
<210>
       145
<211>
       23
<212>
       PRT
<213> Conus magus
<220>
<221>
       PEPTIDE
       (1)..(23)
<222>
<223>
       Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P
       ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
       iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400> 145
Xaa Lys Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Thr Asp
Asn Phe Ile Cys Gly Cys Cys
<210>
       146
<211>
       454
<212>
       DNA
<213>
       Conus magus
<400> 146
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                       60
gettetgttt cecettaetg etetteeaat ggatggagat caacetgeag accaacetge
                                                                      120
agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata agagacaaaa
                                                                      180
gtgttgcggc cccggcggtt catgccccgt atatttcaga gacaatttta tttgtggttg
                                                                      240
ttgttaaatg acaacgtgtc gatgaccatc ttcattatca cgactacgcc aagtgtctaa
                                                                      300
tgaataaata aaatgattgc agtctcgctc agatttgctt ttgtattttg gtctaaagat
                                                                      360
```

caatgaccaa accgttgttt tggtgtggat tttcatatat ttctcgattc ctatccaaca

```
ctagatgatt taatcacgat agatctgatt tttt
                                                                          454
<210>
      147
<211>
      74
<212>
      PRT
<213>
       Conus magus
<400> 147
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
Asp Lys Arg Gln Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys
<210>
      148
      23
<211>
<212> PRT
<213> Conus magus
<220>
<221>
      PEPTIDE
<222>
       (1)..(23)
       Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
       iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400> 148
Xaa Lys Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp
                                      10
Asn Phe Ile Cys Gly Cys Cys
<210>
      149
<211>
      22
<212> PRT
<213> Conus magus
<220>
       PEPTIDE
<221>
<222>
       (1)..(22)
       Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 10 and 20 is
       Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di
       -iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400> 149
Xaa Lys Cys Cys Ser Gly Gly Ser Cys Xaa Leu Xaa Phe Arg Asp Arg
Leu Ile Cys Xaa Cys Cys
            20
<210>
       150
<211>
       19
<212> PRT
```

```
<213> Conus marmoreus
<220>
<221>
       PEPTIDE
       (1)..(19)
<222>
<223>
      Xaa at residue 16 is Pro or Hyp
<400> 150
Ser Lys Gln Cys Cys His Leu Ala Ala Cys Arg Phe Gly Cys Thr Xaa
Cys Cys Asn
<210>
       151
<211>
       321
<212>
      DNA
<213>
      Conus marmoreus
<400> 151
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                       60
gettetgttt ecegttactg etetteegat ggatggtgat caacetgeag acegaettgt
                                                                      120
agagcgtatg caggacaaca tttcatctga gcagcatccc ttctttgaaa agagaagagg
                                                                      180
aggetqttqc acacctccqa qgaaatqcaa agaccqaqcc tqcaaacctq cacqttqctq
                                                                      240
cggcccagga taacgtgttg atgaccaact ttgttatcac ggctacgtca agtgtctagt
                                                                      300
gaataagtaa aacgattgca g
                                                                      321
<210>
      152
<211>
       76
<212>
       PRT
<213>
      Conus marmoreus
<400> 152
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Val Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp
Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
<210> 153
<211> 24
<212> PRT
<213> Conus marmoreus
<220>
<221>
      PEPTIDE
<222>
       (1)..(24)
      Xaa at residue 3, 8, 18 and 24 is Pro or Hyp
<400> 153
Arg Gly Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys
```

```
Lys Xaa Ala Arg Cys Cys Gly Xaa
            20
<210>
       154
<211>
       296
<212>
       DNA
<213>
      Conus marmoreus
<400> 154
gageteggta eccegacete aagagggate gatageagtt catgatgtet aaactgggaa
                                                                       60
tettgttgae catetgteta ettetattte eeettactge tgtteegetg gatggagate
                                                                      120
aacctgcaga ccgacctgca gagcgtatgc aggacgacat ttcatctgaa catcatccct
                                                                      180
tttttgatcc cgtcaaacgg tgttgcaggt tatcatgcgg cctgggatgc cacccttgtt
                                                                      240
gtggatgacc agctttgtta tcgcggcctc atcaagtgtc taatgaataa gtaaaa
                                                                      296
       155
<210>
<211>
       68
<212>
       PRT
<213>
       Conus marmoreus
<400> 155
Met Met Ser Lys Leu Gly Ile Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His His Pro Phe Phe
Asp Pro Val Lys Arg Cys Cys Arg Leu Ser Cys Gly Leu Gly Cys His
Pro Cys Cys Gly
<210>
       156
<211>
       14
<212> PRT
<213> Conus marmoreus
<220>
       PEPTIDE
<221>
<222>
       (1)..(14)
<223>
       Xaa at residue 12 is Pro or Hyp
<400>\ 156
Cys Cys Arg Leu Ser Cys Gly Leu Gly Cys His Xaa Cys Cys
<210>
       157
<211>
       355
<212>
       DNA
      Conus marmoreus
<213>
<400> 157
ggcctacacc aagcttgcat gcctgcaggt cgactctaga ggatccccga tcgatagcag
                                                                       60
ttcatgatgt ctagactggg agtcttgttg accatctgtc tacttctgtt tccccttact
                                                                      120
```

```
gctgttccgc tggatggaga tcaacctgcg gaccgacctg cagagcgcct gcaggacgac
                                                                      180
atttcatctg aacatcatcc ccattttgat tccggcagag agtgttgcgg ttcgttcgca
                                                                      240
tgccgctttg gatgcgtgcc ttgttgtgta tgaccagctt tgttatcacg gcctcatcga
                                                                      300
qtgtctaatg aataagtaaa acgattgcag taggcgggta ccgagctcga attcc
                                                                      355
<210>
       158
<211>
       69
<212>
       PRT
<213> Conus marmoreus
<400> 158
Met Met Ser Arg Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
            20
Ala Glu Arg Leu Gln Asp Asp Ile Ser Ser Glu His His Pro His Phe
Asp Ser Gly Arg Glu Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys
Val Pro Cys Cys Val
65
<210>
       159
<211>
       17
<212>
       PRT
<213>
      Conus marmoreus
<220>
       PEPTIDE
<221>
<222>
       (1)..(17)
<223>
       Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 14 i
       s Pro or Hyp
<400> 159
Xaa Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys
                                     10
Val
<210>
       160
<211>
       295
<212>
       DNA
<213>
       Conus marmoreus
<400> 160
cgacctcaag agggatcgat agcagttcat qatgtctaaa ctqqqaqtct tqttqaccat
                                                                       60
ctgtctactt ctatttcccc ttactgctgt tccgctggat ggagaccaac ctgcagaccg
                                                                      120
acctgcagag cgtatgcagg acgacatttc atctgaacgt catccttttt ttgatcgcag
                                                                      180
caaacagtgt tgccatctgc cggcatgccg cttcggatgt acgccttgtt gttggtgatc
                                                                      240
agctttgtta tcgcgtcctc atcaagtgtc taatgaataa gtaaaatgat tgcag
                                                                      295
<210>
       161
```

<211>

<212>

67

PRT

```
<213> Conus marmoreus
<400> 161
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser His Pro Phe Phe Asp Arg
Ser Lys Gln Cys Cys His Leu Pro Ala Cys Arg Phe Gly Cys Thr Pro
Cys Cys Trp
<210>
       162
<211>
       19
       PRT
<212>
<213> Conus marmoreus
<220>
<221>
      PEPTIDE
<222>
      (1)..(19)
      Xaa at residue 8 and 16 is Pro or Hyp; Xaa at residue 19 is Trp o
<223>
       r bromo-Trp
<400> 162
Ser Lys Gln Cys Cys His Leu Xaa Ala Cys Arg Phe Gly Cys Thr Xaa
Cys Cys Xaa
<210>
       163
<211>
       235
<212>
      DNA
<213>
      Conus marmoreus
<400> 163
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt
                                                                       60
actgetette egetggatgg agateaacet geagaceaac gtgeagageg taegeaggee
                                                                      120
gagaagcatt ccttgcctga tccgagaatg ggctgttgcc cgtttccatg caaaaccagt
                                                                      180
tgcactactt tgtgttgcgg gtgatgataa cgtgttgatg accaactttc tcgag
                                                                      235
<210>
       164
<211>
       67
<212>
       PRT
<213> Conus marmoreus
<400> 164
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp
            20
                                                    30
Gln Arg Ala Glu Arg Thr Gln Ala Glu Lys His Ser Leu Pro Asp Pro
```

Arg Met Gly Cys Cys Pro Phe Pro Cys Lys Thr Ser Cys Thr Thr Leu

```
50
                        55
                                            60
Cys Cys Gly
<210>
       165
<211>
       17
<212>
      PRT
<213>
      Conus marmoreus
<220>
       PEPTIDE
<221>
<222>
      (1)..(17)
     Xaa at residue 5 and 7 is Pro or Hyp
<400> 165
Met Gly Cys Cys Xaa Phe Xaa Cys Lys Thr Ser Cys Thr Thr Leu Cys
Cys
<210>
       166
<211>
       16
<212>
      PRT
<213> Conus marmoreus
<220>
<221>
      PEPTIDE
<222>
      (1)..(16)
<223> Xaa at residue 4 and 6 is Trp or bromo-Trp
<400> 166
Cys Cys His Xaa Asn Xaa Cys Asp His Leu Cys Ser Cys Cys Gly Ser
<210>
       167
<211>
       357
<212>
       DNA
<213>
       Conus marmoreus
<400> 167
gccaagcttg catgcctgca ggatgactct agaggatccc cacctcaaga gggatcgata
                                                                       60
gcagttcatg atgtctaaac tgggagtctt gttgaccatc tgtctacttc tgtttgccct
                                                                      120
tactqctqtt ccqctqqatq qaqatcaacc tqcaqaccqa cctqcaqaac qtatqcaqqa
                                                                      180
cgacatttca tctgaacgtc atcccatgtt tgatgccgtc agagattgtt gcccgttgcc
                                                                      240
ggcatgcccc tttggatgca accettgttg tggatgacca getttgttat egggacetea
                                                                      300
tcaagtgtct aatgaataag taaaaaacga ttcgagtggg taccgagctc gaattcc
                                                                      357
<210>
       168
<211>
       67
<212>
       PRT
<213>
      Conus marmoreus
<400> 168
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Ala Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
                                25
            20
```

```
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser His Pro Met Phe Asp Ala
Val Arg Asp Cys Cys Pro Leu Pro Ala Cys Pro Phe Gly Cys Asn Pro
Cys Cys Gly
<210>
      169
      16
<211>
<212> PRT
<213> Conus marmoreus
<220>
<221> PEPTIDE
<222>
      (1)..(16)
<223> Xaa at residue 4, 6, 9 and 14 is Pro or Hyp <400> 169
Asp Cys Cys Xaa Leu Xaa Ala Cys Xaa Phe Gly Cys Asn Xaa Cys Cys
<210> 170
      16
<211>
<212>
      PRT
<213> Conus marmoreus
<220>
<221>
     PEPTIDE
      (1)..(16)
<223> Xaa at residue 4 and 13 is Pro or Hyp
<400> 170
Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
                                    10
<210> 171
<211> 16
<212> PRT
<213> Conus marmoreus
<220>
     PEPTIDE
<221>
<222>
      (1)..(16)
<223> Xaa at residue 4 and 13 is Pro or Hyp
<400> 171
Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
<210>
       172
<211> 16
<212> PRT
<213> Conus marmoreus
<220>
<221> PEPTIDE
<222>
      (1)..(16)
<223> Xaa at residue 4 and 13 is Pro or Hyp
<400> 172
Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
```

```
<210>
       173
<211>
       17
<212>
      PRT
<213> Conus marmoreus
<220>
       PEPTIDE
<221>
<222>
      (1)..(17)
<223>
      Xaa at residue 14 is Pro or Hyp
<400> 173
Gly Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys
Val
<210>
       174
<211>
       244
<212>
      DNA
<213>
      Conus nobilis
<400> 174
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt
                                                                       60
actgetette egetggatga agateaaceg gtacacegae etgeagageg tatgeaggae
                                                                      120
atttcatctg atcaacatct cttctttgat ctcatcaaac ggtgctgcga gttgccatqc
                                                                      180
gggccaggct tttgcgtccc ttgttgctga catcaataac gtgttgatga ccaactttct
                                                                      240
cgag
                                                                      244
<210>
      175
<211>
       69
<212>
      PRT
<213> Conus nobilis
<400> 175
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Val His
            20
                                                     30
Arg Pro Ala Glu Arg Met Gln Asp Ile Ser Ser Asp Gln His Leu Phe
Phe Asp Leu Ile Lys Arg Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe
    50
                        55
Cys Val Pro Cys Cys
<210> 176
<211>
      15
<212>
      PRT
<213> Conus nobilis
<220>
<221>
      PEPTIDE
<222>
       (1)..(15)
      Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 8
       adn 13 is Pro or Hyp
<400> 176
```

```
Cys Cys Xaa Leu Xaa Cys Gly Xaa Gly Phe Cys Val Xaa Cys Cys
<210>
       177
<211>
       262
<212>
       DNA
<213>
       Conus nobilis
<400> 177
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt
                                                                       60
actgcttttc cgatggatgg agatcaacct gcagaccaac ctgcagatcg tatgcaggac
                                                                      120
gacatttcat ctgagcagta tcccttgttt gataagagac aaaagtgttg cactgggaag
                                                                      180
aaggggtcat gctccggcaa agcatgcaaa aatctcaaat gttgctctgg acgataacgt
                                                                      240
gttgatgacc aactttctcg ag
                                                                      262
<210>
      178
<211>
      78
<212>
      PRT
<213>
       Conus nobilis
<400> 178
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
Leu Phe Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp
Gln Pro Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro
Leu Phe Asp Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys
Ser Gly Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
<210> 179
<211>
       23
      PRT
<212>
<213> Conus nobilis
<220>
<221>
      PEPTIDE
<222>
       (1)..(23)
      Xaa at residue 1 is Gln or pyro-Glu
<400> 179
Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
Lys Asn Leu Lys Cys Cys Ser
<210>
       180
<211>
       238
<212>
       DNA
<213> Conus pulicarius
<400> 180
ggatccatga tgtctaaact gggagttttg ttgaccatct gtctgcttct gtttcccctt
                                                                       60
actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac
                                                                      120
```

```
attgcaactg aacagcatcc cttctttgat cccgtcaaac ggtgttgcaa cagctgttac
                                                                       180
atgggatgca tecettgttg ettetagtaa taacgtgttg atgaccaact ttetegag
                                                                       238
<210>
       181
<211>
       68
<212>
       PRT
<213>
       Conus pulicarius
<400>
       181
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
Arg Pro Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Phe
Phe Asp Pro Val Lys Arg Cys Cys Asn Ser Cys Tyr Met Gly Cys Ile
Pro Cys Cys Phe
<210>
       182
<211>
       14
<212>
      PRT
<213> Conus pulicarius
<220>
<221>
       PEPTIDE
<222>
       (1)..(14)
       Xaa at residue 11 is Pro or Hyp; Xaa at residue 5 is Tyr, 125I-Ty
<223>
       r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400>
       182
Cys Cys Asn Ser Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
<210>
       183
<211>
       238
<212>
       DNA
      Conus quercinus
<400> 183
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt
                                                                        60
acagetette agetggatgg agateaacet geagacegae etgeagageg taegeaggae
                                                                       120
attgcatctg aacagtatcg aaagtttgat cagagacaga ggtgttgcca gtggccatgc
                                                                       180
cccggtagtt gcagatgctg ccgtactggt taacgtgttg atgaccaact ttctcgag
                                                                       238
<210>
       184
<211>
       70
<212>
       PRT
<213>
      Conus quercinus
<400>
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
```

Leu Phe Pro Leu Thr Ala Leu Gln Leu Asp Gly Asp Gln Pro Ala Asp

54 20 25 30 Arg Pro Ala Glu Arg Thr Gln Asp Ile Ala Ser Glu Gln Tyr Arg Lys 40 Phe Asp Gln Arg Gln Arg Cys Cys Gln Trp Pro Cys Pro Gly Ser Cys Arg Cys Cys Arg Thr Gly <210> 185 <211> 17 <212> PRT <213> Conus quercinus <220> <221> PEPTIDE <222> (1)..(17)<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 7 and 9 is Pr o or Hyp; Xaa at residue 6 is Trp or bromo-Trp <400> 185 Xaa Arg Cys Cys Gln Xaa Xaa Cys Xaa Gly Ser Cys Arg Cys Cys Arg 10 Thr <210> 186 <211> 15 <212> PRT <213> Conus quercinus <220> PEPTIDE <221> <222> (1)..(15)<223> Xaa at residue 11 and 14 is Pro or Hyp <400> 186 Cys Cys Ser Gln Asp Cys Leu Val Cys Ile Xaa Cys Cys Xaa Asn <210> 187 <211> 15 <212> PRT <213> Conus quercinus <220> <221> PEPTIDE <222> (1)..(15)Xaa at residue 11 14 is Pro or Hyp; Xaa at residue 7 is Trp or br <223> omo-Trp <400> 187 Cys Cys Ser Arg His Cys Xaa Val Cys Ile Xaa Cys Cys Xaa Asn 10 <210> 188 323 <211>

<400> 188 tcaagaagga tcgatagcag ttcatgatgt ctaaactggg agtcttgttg accatctgtc

<212>

DNA <213> Conus radiatus

tgcttctgtt tccccttact gctcttccga tggatggaga tcaacctgta	gaccgacttg 120
cagagegtat geaggacaae attteatetg ageageatae ettetttgaa	aagagactac 180
catcgtgttg ctcccttaac ttgcggcttt gcccagtacc agcatgcaaa	cgtaaccctt 240
gttgcacagg ataacgtgtt gatgaccaac tttgttatca cggctacgtc	aagtgtctag 300
tgaataagta aaacgattgc agt	323
<210> 189 <211> 76 <212> PRT <213> Conus radiatus	
<400> 189 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu 1 5 10	Leu Phe 15
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Val Asp 20 25 30	Arg Leu
Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Thr 35 40 45	Phe Phe
Glu Lys Arg Leu Pro Ser Cys Cys Ser Leu Asn Leu Arg Leu 50 55 60	Cys Pro
Val Pro Ala Cys Lys Arg Asn Pro Cys Cys Thr Gly 65 70 75	
<210> 190 <211> 24 <212> PRT <213> Conus radiatus	
<220> <221> PEPTIDE <222> (1)(24) <223> Xaa at residue 2, 13, 15 and 21 is Pro or Hyp	
<400> 190 Leu Xaa Ser Cys Cys Ser Leu Asn Leu Arg Leu Cys Xaa Val 1 5 10	. Xaa Ala 15
Cys Lys Arg Asn Xaa Cys Cys Thr 20	
<210> 191 <211> 336 <212> DNA <213> Conus radiatus	
<400> 191 aggtcgactc tagaggatcc ccaaggatcg atagcagttc atgatgtcta	aactgggagt 60
cttgttgacc atctgtctgc ttctgtttcc ccttactgct cttccgatgg	atggagatca 120
acctgcagac cgacttgcag agcgtatgca ggacgacatt tcatctgagc	agcatccctt 180
ctttaaaaag agacaacaaa gatgttgcac cgttaagagg atttgtccag	taccagcatg 240
cagaagtaaa ccttgttgca aatcataacg tattgatgac caactttgtt	atcacggcta 300
cgtcaagtgt ctagtgaata agtaaaatga ttgcag	336

```
<210>
      192
<211>
       75
<212>
      PRT
<213> Conus radiatus
<400> 192
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
                                25
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Phe Phe
Lys Lys Arg Gln Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Pro Val
Pro Ala Cys Arg Ser Lys Pro Cys Cys Lys Ser
<210> 193
<211>
     24
<212> PRT
<213> Conus radiatus
<220>
<221> PEPTIDE
<222>
      (1)..(24)
     Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12, 14 and 20
       is Pro or Hyp
<400> 193
Xaa Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Xaa Val Xaa Ala Cys
Arg Ser Lys Xaa Cys Cys Lys Ser
      194
<210>
<211>
      326
<212>
      DNA
<213>
      Conus radiatus
<400> 194
acctcaagaa ggatcgatag cagttcatga tgtctaaact gggagtcttg ttgaccatct
                                                                      60
gtctgcttct gtttcccgtt actgctcttc cgatggatgg tgatcaacct gcagaccgac
                                                                     120
ttgtagagcg tatgcaggac aacatttcat ctgagcagca tcccttcttt gaaaagagaa
                                                                     180
gaggaggetg ttgcacacct ccgaggaaat gcaaagaccg agcctqcaaa cctgcacqtt
                                                                     240
gctgcggccc aggataacgt gttgatgacc aactttgtta tcacggctac gtcaagtgtc
                                                                     300
tagtgaataa gtaaaacgat tgcagt
                                                                     326
<210>
      195
<211>
       76
<212> PRT
<213> Conus radiatus
<400> 195
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
                                    10
```

```
Pro Val Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp
Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
<210>
      196
<211>
      24
<212> PRT
<213> Conus radiatus
<220>
       PEPTIDE
<221>
<222>
       (1)...(24)
      Xaa at residue 7, 8, 18 and 24 is Pro or Hyp
<400> 196
Arg Gly Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys
                                    10
Lys Xaa Ala Arg Cys Cys Gly Xaa
<210>
      197
<211>
       238
<212>
      DNA
<213>
      Conus rattus
<400> 197
ggatccatga tgtctaaact gggagtcttg gtgaccatct gcctgcttct gttccctctt
                                                                       60
gctgcttttc cactggatgg agatcaacct gcagaccacc ctgcaaagcg tacgcaagat
                                                                      120
gacagttcag ctgccctgat caatgcctgg cttgatgaat cccagacttg ctgcagtaac
                                                                      180
tgcggtgaag attgtgatgg ttgttgccag taacgtgttg atgaccaact ttctcgag
                                                                      238
<210>
       198
<211>
       70
<212>
       PRT
<213>
      Conus rattus
<400> 198
Gly Ser Met Met Ser Lys Leu Gly Val Leu Val Thr Ile Cys Leu Leu
Leu Phe Pro Leu Ala Ala Phe Pro Leu Asp Gly Asp Gln Pro Ala Asp
His Pro Ala Lys Arg Thr Gln Asp Asp Ser Ser Ala Ala Leu Ile Asn
                            40
Ala Trp Leu Asp Glu Ser Gln Thr Cys Cys Ser Asn Cys Gly Glu Asp
Cys Asp Gly Cys Cys Gln
```

```
<210>
       199
       16
<211>
<212>
       PRT
<213>
      Conus rattus
<220>
<221>
       PEPTIDE
<222>
       (1)..(16)
      Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 9 is Glu or q
       amma-carboxy Glu
<400>
       199
Xaa Thr Cys Cys Ser Asn Cys Gly Xaa Asp Cys Asp Gly Cys Cys Gln
<210>
       200
<211>
       327
<212>
       DNA
<213>
       Conus stercusmuscarum
<400> 200
gacctcaaga qqqatcqata qcaqttcqtq atqtctaaac tqqqaqtctt qttqaccatc
                                                                       60
tgtctgcttc tgtttcctct tactgctctt ccgatggatg gagatcaacc tgcagaccaa
                                                                      120
cctgcagatc gtatgcagga cgacatttca tctgagcagt atcccttgtt tgataagaga
                                                                      180
caaaagtgtt gcactgggaa gaaggggtca tgctccggca aagcatgcaa aaatctcaaa
                                                                      240
tgttgctctg gacgataacg tgttgatgac caactttgtt atcacggcta cgtcaagtgt
                                                                      300
ctaatgaata agtaaaacga ttgcagt
                                                                      327
<210>
       201
<211>
       75
<212>
       PRT
<213>
      Conus stercusmuscarum
<400> 201
Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe Pro
Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro Ala
            20
                                25
                                                     30
Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe Asp
Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys
Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
<210>
       202
<211>
       23
<212>
      PRT
<213>
      Conus stercusmuscarum
<220>
<221>
       PEPTIDE
<222>
       (1)..(23)
<223>
      Xaa at residue 1 is Gln or pyro-Glu
<400> 202
Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
```

```
1
                                   10
                                                      15
Lys Asn Leu Lys Cys Cys Ser
           20
<210>
      203
<211>
       316
<212>
      DNA
<213>
       Conus stercusmuscarum
<400>
       203
gategatage agttegtgat gtetaaactg ggagtettgt tgaccatetg tetgettetg
                                                                    60
tttcccctta ctgctcttcc gatggatgga gatcaacctg cagaccaacc tgcagatcgt
                                                                   120
atgcagaacg acatttcatc tgagcagtat cccttgtttg ataagagaca aaagtgttgc
                                                                   180
ggccccggcg cgtcatgccc cagatatttc aaagacaatt ttatttgtgg ttgttgttaa
                                                                   240
atgacaacgt gtcgatgacc aacttcgtta tcacgacttc gccaagtgtc taatgaataa
                                                                   300
gtaaaacgat tgcagt
                                                                   316
<210>
      204
      73
<211>
<212>
      PRT
<213>
      Conus stercusmuscarum
<400> 204
Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe Pro
Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro Ala
Asp Arg Met Gln Asn Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe Asp
Lys Arg Gln Lys Cys Cys Gly Pro Gly Ala Ser Cys Pro Arg Tyr Phe
Lys Asp Asn Phe Ile Cys Gly Cys Cys
<210>
      205
<211>
      23
<212>
      PRT
<213> Conus stercusmuscarum
<220>
<221>
      PEPTIDE
<222>
      (1)..(23)
<223>
      Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P
      ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
       iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400> 205
Asn Phe Ile Cys Gly Cys Cys
<210>
       206
<211>
       331
<212>
      DNA
```

```
<213> Conus striatus
<400> 206
cgacctttca agagggatcg atagcagttc gcgatgtcta aactgggggt attgttgacc
                                                                        60
atctgtctgc ttctgtttcc ccttactgct cttccgatgg atgaagatca acctgcagac
                                                                       120
caacttgaag atcgtatgca ggacgacatt tcatctgagc agtatccctc `gtttgttagg
                                                                       180
agacaaaagt gttgcggcga aggctcgtca tgccccaaat atttcaaaaa caattttatt
                                                                       240
tgtggttgtt gttaaatgac aacgtgtcga tgaccaactt cgttatcacq actacqccaa
                                                                       300
gtgtcttgtc taatgataat aaaatgattc c
                                                                       331
<210>
       207
<211>
       73
<212>
       PRT
<213>
       Conus striatus
<400> 207
Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe Pro
Leu Thr Ala Leu Pro Met Asp Glu Asp Gln Pro Ala Asp Gln Leu Glu
Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Ser Phe Val
        35
                            40
Arg Arg Gln Lys Cys Cys Gly Glu Gly Ser Ser Cys Pro Lys Tyr Phe
Lys Asn Asn Phe Ile Cys Gly Cys Cys
<210>
       208
<211>
       23
<212>
       PRT
<213>
       Conus striatus
<220>
<221>
       PEPTIDE
<222>
       (1)..(23)
<223>
       Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 is Glu or g
       amma-carboxy Glu; Xaa at residue 11 is Pro or Hyp; Xaa at residue
        13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
        O-phospho-Tyr
<400> 208
Xaa Lys Cys Cys Gly Xaa Gly Ser Ser Cys Xaa Lys Xaa Phe Lys Asn
                                     10
Asn Phe Ile Cys Gly Cys Cys
<210>
       209
<211>
       256
<212>
       DNA
<213>
      Conus striatus
<400> 209
ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttcccctt
                                                                        60
actgctcttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac
                                                                       120
```

```
gacatttcat ctgacgagca tcccttgttt gataagagac aaaactgttg caatggggga
                                                                       180
tgctccagca aatggtgcag agatcacgca cgttgttgcg gtcgatgata acgtgttqat
                                                                       240
gaccaacttt ctcgag
                                                                       256
<210>
       210
<211>
       75
<212>
       PRT
<213>
       Conus striatus
<400> 210
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu
Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp
            20
Arg Pro Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Asp Glu His Pro
                             40
Leu Phe Asp Lys Arg Gln Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys
Trp Cys Arg Asp His Ala Arg Cys Cys Gly Arg
                    70
<210>
       211
<211>
       20
<212>
      PRT
<213> Conus striatus
<220>
<221>
       PEPTIDE
<222>
       (1)..(20)
       Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 is Trp or
<223>
       bromo-Trp
<400> 211
Xaa Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys Xaa Cys Arg Asp His
                                     10
Ala Arg Cys Cys
<210>
       212
<211>
       235
<212>
       DNA
<213>
       Conus tessulatus
<400> 212
ggatccatga tgtctaaact gggagtcttg ttgaccatgt gtctgcttct qtttcccctt
                                                                        60
actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg taggcaggac
                                                                       120
attgcaactg acgatcatcc tttgtttgat cccgtcaaac ggtgctgcca caaatgctat
                                                                       180
atgggatgca tcccttgttg catttagtaa cgtgttgatg accaactttc tcgag
                                                                       235
<210>
       213
<211>
       68
<212>
       PRT
<213>
       Conus tessulatus
<400>
       213
```

```
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Met Cys Leu Leu
Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
Arg Pro Ala Glu Arg Arg Gln Asp Ile Ala Thr Asp Asp His Pro Leu
Phe Asp Pro Val Lys Arg Cys Cys His Lys Cys Tyr Met Gly Cys Ile
    50
                        55
Pro Cys Cys Ile
<210>
       214
<211>
       14
<212>
       PRT
<213> Conus tessulatus
<220>
<221>
       PEPTIDE
<222>
       (1)..(14)
       Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Ty
       r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400>
       214
Cys Cys His Lys Cys Xaa Met Gly Cys Ile Xaa Cys Cys Ile
<210>
       215
<211>
       238
<212>
       DNA
<213>
      Conus tessulatus
<400> 215
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtgtgcttct gtttcccctt
                                                                       60
actgctgttc cgctggatgg agatcaacct gcagaccaac ctgcagagcg tacqcagaac
                                                                      120
gagcagcatc ccttgtatga tcagaaaaga aagtgttgcc ggccgccatg cgccatgagc
                                                                      180
tgcggcatgg ctaggtgttg ctattaatga taacgtgttg atgaccaact ttctcgag
                                                                      238
<210>
       216
<211>
       68
<212>
       PRT
<213>
      Conus tessulatus
<400> 216
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Val Leu
Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
Gln Pro Ala Glu Arg Thr Gln Asn Glu Gln His Pro Leu Tyr Asp Gln
        35
Lys Arg Lys Cys Cys Arg Pro Pro Cys Ala Met Ser Cys Gly Met Ala
                        55
Arg Cys Cys Tyr
```

```
<210>
       217
<211>
      18
<212>
      PRT
<213> Conus tessulatus
<220>
<221>
       PEPTIDE
<222>
       (1)..(18)
      Xaa at residue 5 and 6 is Pro or Hyp; Xaa at residue 18 is Tyr, 1
       25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 217
Lys Cys Cys Arg Xaa Xaa Cys Ala Met Ser Cys Gly Met Ala Arg Cys
Cys Xaa
<210>
       218
<211>
       564
<212>
       DNA
<213>
      Conus textile
<400> 218
qaqtcaaccc actqtcacqc caaqaqcqqa cqccacaqct aaqqcaaqaa qqatcqataq
                                                                       60
cagttcatga tgtctaaact gggagccttg ttgaccatct gtctacttct gttttccctt
                                                                      120
actgctgttc cgctggatgg agatcaacat gcagaccaac ctgcacagcg tctgcaggac
                                                                      180
cgcattccaa ctgaagatca tcccttattt gatcccaaca aacggtgttg cccgccqgtq
                                                                      240
gcatgcaaca tgggatgcaa gccttgttgt ggatgaccag ctttgttatc gcggtctcat
                                                                      300
gaagtgtcta atgaataagt aaaacgattg cagtttcgtt cagatttgct gttgtatttt
                                                                      360
ggtctaaaga ttaatgacca aactgttctt ttgatccgga ttttcacgta tttctcgatt
                                                                      420
cctattcaac actagataag ttaatcacga cagatctgat tttccatcaa tgccttgctt
                                                                      480
tttggtctgt catataaatc ttgtttatat ttaatttctc gtcactttca acacgcacac
                                                                      540
acacacaca acacacgege gege
                                                                      564
<210>
       219
<211>
       69
<212>
       PRT
<213>
      Conus textile
<400> 219
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Phe
Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
Ala Gln Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe
                            40
Asp Pro Asn Lys Arg Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys
Lys Pro Cys Cys Gly
```

```
<210>
       220
<211>
       16
       PRT
<212>
<213> Conus textile
<220>
<221>
       PEPTIDE
<222>
       (1)..(16)
<223>
      Xaa at residue 3, 4 and 13 is Pro or Hyp
<400>
       220
Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Lys Xaa Cys Cys Gly
<210>
       221
<211>
       780
<212>
       DNA
<213>
       Conus textile
<400> 221
qqatccaqac qacaaaqaaq aqtcaaccca ctqccacqtc aaqaqcaqaq cccacaqcta
                                                                       60
agacaagaag gatcgatagc agttcatgat gtttaaactg ggagtcttgt tgaccatctg
                                                                      120
tctccttctg ttttccctta atgctgttcc gttggatgga gatcaacctg cagaccaacc
                                                                      180
tgcagagcgt ctgctggacg acatttcatt tgaaaataat cccttttatg atcccqccaa
                                                                      240
acggtgttgc aggacttgct tcggttgcac accttgttgt ggatgaccag cctcatcaag
                                                                      300
tgtctaacga ataagtaaag cgattgcagt ctcgttcaga tttacttttg tattctgqtc
                                                                      360
taaagattaa tgaccaaact cttcttttga tccggatgta catatatttc tcgattccta
                                                                      420
tccaacgcta gataagctaa tcacgacaga tctgattttc tgtcaatgcc ttgctttttg
                                                                      480
gtctctcata tcactcttgt ttatatttaa tttctcgtca ctatatatat atatacacac
                                                                      540
acacacaca ggaattccga ttgtccagta ccgttcttgg gatcgaggta ttgctgcgat
                                                                      600
ggcttattct gtactctttt cttctgcgct tgatagtgat gtcttctact cccatctqtq
                                                                      660
ctacccctgg cttgatcttt gataggcgtg tgcccttcac tggttataaa cccctctgat
                                                                      720
cctactctct ggacgcctcg ggggcccaac ctccaaataa agcgacatcc aatgaaaaaa
                                                                      780
<210>
       222
<211>
       66
<212>
       PRT
<213>
       Conus textile
<400> 222
Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Ser Leu Asn Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
Ala Glu Arg Leu Leu Asp Asp Ile Ser Phe Glu Asn Asn Pro Phe Tyr
Asp Pro Ala Lys Arg Cys Cys Arg Thr Cys Phe Gly Cys Thr Pro Cys
```

Cys Gly

```
65
<210>
       223
      12
<211>
<212>
      PRT
<213> Conus textile
<220>
<221>
       PEPTIDE
<222>
       (1)..(12)
      Xaa at residue 10 is Pro or Hyp
<223>
<400> 223
Cys Cys Arg Thr Cys Phe Gly Cys Thr Xaa Cys Cys
<210>
       224
<211>
       456
<212>
       DNA
      Conus textile
<213>
<400> 224
ggaacagtca accccacagc cacgccaaga gcagacagcc acagctacgt gaagaagggt
                                                                       60
ggagagaggt tcatgatgtt gaaaatggga gtggtgctat tcatctttct ggtactgttt
                                                                      120
cccctggcaa cgctccagct ggatgcagat caacctgtag aacgatatgc ggagaacaaa
                                                                      180
cageteetea acceagatga aaggagggaa atcetattge etgetetgag gaagttetge
                                                                      240
tqtqattcqa attqqtqcca catttcqqat tqtqaqtqct qctacqqtta qcqccqaaca
                                                                      300
tocatggcac tgtgctgggc ggtttcatcc caacaacgac agcgtttgtt gatttcatgt
                                                                      360
atcattgcgc ccacgtctct tgtctaagaa tgacgaacat gattgcactc tggttcagat
                                                                      420
ttcgtgttct tttctgacaa taaatgacaa acctcc
                                                                      456
<210>
       225
<211>
      70
<212>
       PRT
<213>
      Conus textile
<400> 225
Met Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe
Pro Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr
            20
Ala Glu Asn Lys Gln Leu Leu Asn Pro Asp Glu Arg Arg Glu Ile Leu
Leu Pro Ala Leu Arg Lys Phe Cys Cys Asp Ser Asn Trp Cys His Asp
Cys Glu Cys Cys Tyr Gly
65
<210>
       226
<211>
       17
<212>
       PRT
<213> Conus textile
<220>
```

.20/

```
<221>
      PEPTIDE
<222>
       (1)..(17)
<223>
     Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 7 i
       s Trp or bromo-Trp; Xaa at residue 17 is Tyr, 125I-Tyr, mono-iodo
       -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400> 226
Phe Cys Cys Asp Ser Asn Xaa Cys His Ile Ser Asp Cys Xaa Cys Cys
Xaa
<210> 227
<211>
      456
<212> DNA
<213> Conus textile
<220>
<221>
      misc feature
      (1)..(456)
<222>
       n may be any nucleotide
<400> 227
caaggaacag tcaaccccac agccacgcca agagcagaca gccacagcta cgtgaagaag
                                                                       60
ggtggagaga ggttcgtgat gttgaaaatg ggagtggtgc tattcatctt cctgqtactq
                                                                      120
tttcccctgg caacgctcca gctggatgca gatcaacctg tagaacgata tgcggagaac
                                                                      180
aaacagetee teageecaga tgaaaggagg gaaateatat tgeatgetet qgqqaeqeqa
                                                                      240
tgctgttctt gggatgtgtg cgaccacccg agttgtactt gctgcggtta gcgccgaaca
                                                                      300
tccatggcgc tgtgctgggc ggttttatcc caacaacgac agcgtttgtt gatttcatgt
                                                                      360
atcattgcgc ccacgtctct tgtctaagaa tgacgaacat gattgcactc tggttcagat
                                                                      420
ttcgtgttct tttctgacaa taaatgacaa aacncc
                                                                      456
<210>
       228
<211>
       70
<212>
       PRT
<213> Conus textile
<400> 228
Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe Pro
Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr Ala
Glu Asn Lys Gln Leu Leu Ser Pro Asp Glu Arg Arg Glu Ile Ile Leu
His Ala Leu Gly Thr Arg Cys Cys Ser Trp Asp Val Cys Asp His Pro
Ser Cys Thr Cys Cys Gly
       229
<210>
<211>
       15
<212>
       PRT
<213> Conus textile
```

```
<220>
<221>
       PEPTIDE
<222>
       (1)..(15)
       Xaa at residue 10 is Pro or Hyp; Xaa at residue 4 is Trp or bromo
       -Trp
<400> 229
Cys Cys Ser Xaa Asp Val Cys Asp His Xaa Ser Cys Thr Cys Cys
                                     10
<210>
       230
<211>
      235
<212>
      DNA
<213> Conus textile
<400> 230
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt
                                                                        60
actgetette egetggatgg agateaacce geagaceaag etgeagageg tatgeaggee
                                                                      120
gagcagcatc ccttgtttga tcagaaaaga cggtgctgca agtttccatg ccccqatagt
                                                                      180
tgcagatatt tgtgttgcgg gtgatgataa cgtgttgatg accaactttc tcgag
                                                                      235
<210>
       231
       67
<211>
<212>
       PRT
<213> Conus textile
<400> 231
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp
            20
Gln Ala Ala Glu Arg Met Gln Ala Glu Gln His Pro Leu Phe Asp Gln
Lys Arg Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Arg Tyr Leu
Cys Cys Gly
       232
<210>
<211>
       16
<212>
       PRT
<213>
      Conus textile
<220>
<221>
       PEPTIDE
<222>
       (1)..(16)
       Xaa at residue 3 and 8 is Pro or Hyp; Xaa at residue 13 is Tyr, 1
       25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 232
Arg Cys Cys Lys Phe Xaa Cys Xaa Asp Ser Cys Arg Xaa Leu Cys Cys
<210>
       233
<211>
       321
<212>
       DNA
```

```
<213> Conus tulipa
<400>
       233
cgacctcaag agggatcgat agcagttcat gtctaaactg ggagtcttgt tgacaatctg
                                                                       60
totgottotg tttcccctta ctgctctqcc qatqqatqqa qatqaacctq caqaccqacc
                                                                      120
tgcagagcgt atgcaggaca acatttcatc tgagcagcat cccttgtttg aggagagaca
                                                                      180
cggatgttgc aaggggcccg aaggatgctc ctccaqaqaa tqcaqacccc aacattgttg
                                                                      240
cggtcgacga taacgtgttg agggccaact ttgttatcac ggctacgtca agtgtttagt
                                                                      300
gaataagtaa aatgattgca g
                                                                      321
<210>
       234
<211>
       74
<212>
       PRT
<213>
      Conus tulipa
<400> 234
Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe Pro
Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asp Arg Pro Ala
Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Leu Phe Glu
Glu Arg His Gly Cys Cys Lys Gly Pro Glu Gly Cys Ser Ser Arg Glu
Cys Arg Pro Gln His Cys Cys Gly Arg Arg
<210>
      235
<211>
      21
<212>
      PRT
<213>
      Conus tulipa
<220>
       PEPTIDE
<221>
<222>
      (1)..(21)
      Xaa at residue 8 and 14 is Glu or gamma-carboxy Glu; Xaa at resid
       ue 7 and 17 is Pro or Hyp
<400> 235
His Gly Cys Cys Lys Gly Xaa Xaa Gly Cys Ser Ser Arg Xaa Cys Arg
Xaa Gln His Cys Cys
<210>
       236
<211>
       287
<212>
       DNA
<213>
      Conus figulinus
caaqaaqqat cqataqcaqt tcatqatqtc taaactqqqa qtcttqctqa ccatctqtct
                                                                       60
gcttctgatt ccccttactg ctctttcgct ggatggagat caacctgcag accgacctgc
                                                                      120
```

agagcgtatg caggatggaa tttcatctga acagcatccc atgtttgatc ccgtcagacg

```
gtgttgcccg tggccatgca acataggatg cgtaccttgt tgttgatgac cagttttqtt
                                                                      240
atcgcggcct catcaaatgt ctaatgaata agtaaaacga ttgcagt
                                                                      287
<210>
       237
<211>
       67
<212>
       PRT
<213>
      Conus figulinus
<400> 237
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Ile
                                    10
Pro Leu Thr Ala Leu Ser Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu Gln His Pro Met Phe
Asp Pro Val Arg Arg Cys Cys Pro Trp Pro Cys Asn Ile Gly Cys Val
Pro Cys Cys
<210>
       238
<211>
<212>
       PRT
<213> Conus figulinus
<220>
      PEPTIDE
<221>
<222>
       (1)..(14)
      Xaa at residue 3, 5 and 12 is Pro or Hyp; Xaa at residue 4 is Trp
<223>
        or bromo-Trp
<400> 238
Cys Cys Xaa Xaa Xaa Cys Asn Ile Gly Cys Val Xaa Cys Cys
<210>
       239
<211>
       283
<212>
       DNA
<213>
      Conus figulinus
<400> 239
caagagggat cgatagcagt tcatgatgtt taaactggga gtcctgttga ccatctgtat
                                                                       60
gettetgttt ccctttactg ctcttccgct ggatggagag caacctgcag accaacctgc
                                                                      120
agagegeatg cagtatgaca tgttacgtgc aatgaatece tggtttgate cegteaaaaq
                                                                      180
gtgctgctcg aagaactgcg cagtatgcat cccttgttgc ccgtaactga ccagcttgat
                                                                      240
tatcgcggcc aaggctctaa tgaataagta aaacgattgc agt
                                                                      283
<210>
       240
<211>
       67
<212>
       PRT
<213>
      Conus figulinus
<400>
       240
Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Met Leu Leu Phe
                                    10
Pro Phe Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Ala Asp Gln Pro
```

20 25 30 Ala Glu Arg Met Gln Tyr Asp Met Leu Arg Ala Met Asn Pro Trp Phe Asp Pro Val Lys Arg Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Pro Cys Cys Pro <210> 241 <211> 14 <212> PRT <213> Conus figulinus <220> <221> PEPTIDE <222> (1)..(14)Xaa at residue 11 and 14 is Pro or Hyp <400> 241 Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Xaa Cys Cys Xaa <210> 242 <211> 286 <212> DNA <213> Conus figulinus <400> 242 caagagggat cgatagcagt tcatgatgtc taaactgaga gtcttgttga ccttatgtct 60 gcttctgttt ccccttactg ctcttccgct gaatgaagat caacctgcag agcgtatgca 120 ggacgacaat tcatctgagc agcacccctt gtatgaccac aaacgaaagt gttgccqgtg 180 gccatgcccc gcaagatgcg gctcttgttg cctgtaataa cgtgttggcc aactttgtta 240 tcacggccac gtcaaatgtt taatgaataa gtaaaacgat tgcagt 286 <210> 243 <211> 64 <212> PRT <213> Conus figulinus <400> 243 Met Met Ser Lys Leu Arg Val Leu Leu Thr Leu Cys Leu Leu Phe Pro Leu Thr Ala Leu Pro Leu Asn Glu Asp Gln Pro Ala Glu Arg Met Gln Asp Asp Asn Ser Ser Glu Gln His Pro Leu Tyr Asp His Lys Arg Lys Cys Cys Arg Trp Pro Cys Pro Ala Arg Cys Gly Ser Cys Cys Leu 55 50 <210> 244 <211> 15 <212> PRT <213> Conus figulinus

<220>

```
<221>
      PEPTIDE
<222>
       (1)..(15)
      Xaa at residue 5 and 7 is Pro or Hyp; Xaa at residue 4 is Trp or
       bromo-Trp
<400> 244
Cys Cys Arg Xaa Xaa Cys Xaa Ala Arg Cys Gly Ser Cys Cys Leu
<210>
       245
       301
<211>
<212>
       DNA
<213> Conus figulinus
<400> 245
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccttatgtct
                                                                       60
gettetgttt cecetgactg etetteeget ggatgaagat caagetgeag accgaectge
                                                                     120
agagegtatg cagggeatgt catetgaaca geatecette tttgateeeg teaaacqqtq
                                                                     180
ttgcgagttg tcacgctgcc ttggatgcgt cccttgttgc acatcttaat aacgtgtgga
                                                                     240
tgaccaactg tgttatcacg gccacgtcaa gtgtctaatg aataagtaaa atgattgcag
                                                                     300
t
                                                                     301
<210> 246
<211>
      68
<212>
      PRT
<213> Conus figulinus
<400> 246
Met Met Ser Lys Leu Gly Val Leu Leu Thr Leu Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Ala Ala Asp Arg Pro
Ala Glu Arg Met Gln Gly Met Ser Ser Glu Gln His Pro Phe Asp
Pro Val Lys Arg Cys Cys Glu Leu Ser Arg Cys Leu Gly Cys Val Pro
                        55
Cys Cys Thr Ser
<210>
      247
<211>
       16
<212>
       PRT
<213>
     Conus figulinus
<220>
<221>
       PEPTIDE
<222>
      (1)..(16)
<223> Xaa at residue 3 and 12 is Pro or Hyp
<400> 247
Cys Cys Xaa Leu Ser Arg Cys Leu Gly Cys Val Xaa Cys Cys Thr Ser
                                    10
<210>
       248
<211>
       301
<212>
      DNA
```

```
<213> Conus figulinus
<400> 248
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccttatgtct
                                                                       60
gettetgttt cecetgactg etetteeget ggatgaagat caacetgeag accgaeetge
                                                                      120
agagegtatg cagggeatgt catetgaaca geatecette tttgateeeg teaaaeggtg
                                                                      180
ttgcgagttg tcaaaatgcc atggatgcgt cccttgttgc ataccttaat aacgtgcgga
                                                                      240
tgaccaactg tgttatcacg gccacgtcaa gtgtctaatg aataagtaaa atgattgcag
                                                                      300
                                                                      301
<210>
       249
<211>
       68
<212>
       PRT
<213>
      Conus figulinus
<400> 249
Met Met Ser Lys Leu Gly Val Leu Leu Thr Leu Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
Ala Glu Arg Met Gln Gly Met Ser Ser Glu Gln His Pro Phe Phe Asp
Pro Val Lys Arg Cys Cys Glu Leu Ser Lys Cys His Gly Cys Val Pro
    50
                        55
                                            60
Cys Cys Ile Pro
65
<210>
       250
<211>
       16
<212>
       PRT
<213> Conus figulinus
<220>
       PEPTIDE
<221>
<222>
       (1)..(16)
       Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 12 a
       nd 16 is Pro or Hyp
<400>
       250
Cys Cys Xaa Leu Ser Lys Cys His Gly Cys Val Xaa Cys Cys Ile Xaa
<210>
       251
       298
<211>
<212>
       DNA
<213>
       Conus quercinus
<400> 251
caagagggat cgatagcagt tcatgatgtc taaactcgga gtcttgttga ccatctgtct
                                                                       60
ggttctgttt ccccttacag ctcttcagct ggatggagat caacctgcag accgacctgc
                                                                      120
agagcgtacg caggacattt catctgaaca gtatcgaaag tttgatcaga gacagaggtg
                                                                      180
ttgccggtgg ccatgcccg gtagttgcag atgctgccgt tatcgttaac gtgttggtga
                                                                      240
ccagctttgt tatcacgacc acgccaagtg tctaacgaat aagtaaaatg attgcagt
                                                                      298
```

```
<210>
       252
<211>
       68
<212>
       PRT
<213>
       Conus quercinus
<400> 252
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val Leu Phe
Pro Leu Thr Ala Leu Gln Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
Ala Glu Arg Thr Gln Asp Ile Ser Ser Glu Gln Tyr Arg Lys Phe Asp
Gln Arg Gln Arg Cys Cys Arg Trp Pro Cys Pro Gly Ser Cys Arg Cys
Cys Arg Tyr Arg
<210>
       253
<211>
       18
<212>
       PRT
<213>
       Conus quercinus
<220>
<221>
       PEPTIDE
<222>
       (1)..(18)
<223>
       Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 7 and 9 is Pr
       o or Hyp; Xaa at residue 6 is Trp or bromo-Trp; Xaa at residue 17
        is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-
       phospho-Tyr
<400> 253
Xaa Arg Cys Cys Arg Xaa Xaa Cys Xaa Gly Ser Cys Arg Cys Cys Arg
Xaa Arg
<210>
       254
<211>
       313
<212>
       DNA
<213>
       Conus quercinus
<400> 254
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                        60
gcttctgttt ccccttactg ctcttccact ggatggagat caacctgcag atcaatctgc
                                                                       120
agagcgacct gcagagcgta cgcaggacga cattcagcag catccgttat atgatccgaa
                                                                       180
aagaaggtgt tgccgttatc catgccccga cagctgccac ggatcttgct gctataagtg
                                                                       240
ataacatgtt gatggccagc tttgttatca cggccacgtc aagtgtctaa tgaataagta
                                                                       300
aaacgattgc agt
                                                                       313
<210>
       255
<211>
       72
<212>
       PRT
<213>
       Conus quercinus
<400>
       255
```

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Ser Ala Glu Arg Pro Ala Glu Arg Thr Gln Asp Asp Ile Gln Gln His Pro Leu Tyr Asp Pro Lys Arg Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser 50 55 60 Cys His Gly Ser Cys Cys Tyr Lys <210> 256 <211> 18 <212> PRT <213> Conus quercinus <220> PEPTIDE <221> <222> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 and 17 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos pho-Tyr <400> 256 Arg Cys Cys Arg Xaa Xaa Cys Xaa Asp Ser Cys His Gly Ser Cys Cys Xaa Lys <210> 257 <211> 256 <212> DNA <213> Conus wittigi <400> 257 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccatt 60 actgctcttc cggtgggtgg agatcagcct gcagaccgac ttgcagagcg tatgcaggac 120 gacacttcat ctgagcagca tccctttgaa aagagactac catcatgttg cgactttgag 180 aggetttgeg tagtaceage atgeataegt cateagtgtt geacaggata aegtgttgat 240 gaccaacttt ctcgag 256 <210> 258 <211> 74 <212> PRT <213> Conus wittigi <400> 258 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe Pro Ile Thr Ala Leu Pro Val Gly Gly Asp Gln Pro Ala Asp Arg Leu 20 25 30 Ala Glu Arg Met Gln Asp Asp Thr Ser Ser Glu Gln His Pro Phe Glu Lys Arg Leu Pro Ser Cys Cys Asp Phe Glu Arg Leu Cys Val Val Pro

```
Ala Cys Ile Arg His Gln Cys Cys Thr Gly
                    70
<210>
       259
<211>
      23
<212>
      PRT
<213> Conus wittigi
<220>
<221>
      PEPTIDE
<222>
      (1)..(23)
<223> Xaa at residue 8 is Glu or gamma-carboxy Glu; Xaa at residue 2 an
       d 14 is Pro or Hyp
<400>
      259
Leu Xaa Ser Cys Cys Asp Phe Xaa Arg Leu Cys Val Val Xaa Ala Cys
Ile Arg His Gln Cys Cys Thr
            20
<210> 260
<211>
      14
<212>
      PRT
<213>
      Conus betulinus
<220>
<221>
      PEPTIDE
<222>
      (1)...(14)
<223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 14 is Trp or brom
       o-Trp
<400> 260
Cys Cys Lys Gln Ser Cys Thr Thr Cys Met Xaa Cys Cys Xaa
<210>
      261
<211>
       259
<212>
      DNA
<213> Conus tulipa
<220>
<221>
      misc_feature
      (1)...(259)
<222>
<223> n may be any nucleotide
<400> 261
ggatccatga tgtctaaact gggagtcttg ttgacaatct gtctgcttct gtttcccctt
                                                                      60
actgctctgc cgatggatgg agatgaacct gcagaccgac ctgcagagcg tatgcaggac
                                                                     120
aacatttcat ctgagcagca tcccttgttt gaggagagac acggatgttg cgaggggccg
                                                                     180
aagggatgct cctccagaga atgcagaccc caacattgtt gcggtcgacg ataacgtgtt
                                                                     240
gatgaccaac tntctcgag
                                                                     259
<210>
       262
<211>
       75
<212>
      PRT
<213> Conus tulipa
<400>
      262
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
```

```
1
                                     10
                                                         15
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asp Arg Pro
            20
Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Leu Phe
Glu Glu Arg His Gly Cys Cys Glu Gly Pro Lys Gly Cys Ser Ser Arg
Glu Cys Arg Pro Gln His Cys Cys Gly Arg Arg
<210>
       263
<211>
       21
<212>
       PRT
<213>
      Conus tulipa
<220>
<221>
       PEPTIDE
<222>
       (1)..(21)
<223>
       Xaa at residue 5 and 14 is Glu or gamma-carboxy Glu; Xaa at resid
       ue 7 and 17 is Pro or Hyp
<400> 263
His Gly Cys Cys Xaa Gly Xaa Lys Gly Cys Ser Ser Arg Xaa Cys Arg
                                    10
Xaa Gln His Cys Cys
            20
<210>
       264
<211>
       262
<212>
      DNA
<213> Conus aurisiacus
<220>
<221>
      misc feature
<222>
      (1)..(262)
<223>
      n may be any nucleotide
<400> 264
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt
                                                                       60
actgcttttc cgatggatgg agatcaacct gcagaccaac ctgcagatcg tatgcaggac
                                                                      120
gacatttcat ctgagcagta tcccttgttt gataagagac aaaagtgttg cactgggagg
                                                                      180
aaggggtcat gctccggcaa agcatgcaaa aatctcaaat gttgctctqg acgataacqt
                                                                      240
gttgatgacc aactttctcg an
                                                                      262
<210>
       265
<211>
       76
<212>
      PRT
<213> Conus aurisiacus
<400> 265
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
            20
                                25
```

```
Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
Asp Lys Arg Gln Lys Cys Cys Thr Gly Arg Lys Gly Ser Cys Ser Gly
Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
<210>
       266
<211>
       23
<212>
      PRT
<213> Conus aurisiacus
<220>
<221>
      PEPTIDE
<222>
       (1)..(23)
      Xaa at residue 1 is Gln or pyro-Glu
<400> 266
Xaa Lys Cys Cys Thr Gly Arg Lys Gly Ser Cys Ser Gly Lys Ala Cys
                                    10
Lys Asn Leu Lys Cys Cys Ser
<210>
       267
<211>
       239
<212>
       DNA
     Conus betulinus
<213>
<400> 267
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct qtttcccctt
                                                                       60
actgctgttc cgttggatgg agatcaacct gcagaccaac ctgcagagcg tatgcagaac
                                                                      120
gagcagcatc cctcgtttga tcagaaaaga aggtgctgcc ggtggccatq ccccagtata
                                                                      180
tgcggcatgg ctaggtgttg cttcgtcatg ataacgtgtt gatgaccaac tttctcgag
                                                                      239
<210>
       268
<211>
       71
<212>
       PRT
<213>
      Conus betulinus
<400> 268
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
Ala Glu Arg Met Gln Asn Glu Gln His Pro Ser Phe Asp Gln Lys Arg
                            40
Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
                        55
Cys Phe Val Met Ile Thr Cys
<210>
       269
<211>
       23
<212>
      PRT
<213> Conus betulinus
```

```
<220>
<221>
       PEPTIDE
<222>
       (1)..(23)
<223>
      Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or
       bromo-Trp
<400> 269
Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Ile Cys Gly Met Ala Arg Cys
Cys Phe Val Met Ile Thr Cys
            20
<210>
       270
<211>
       226
<212>
      DNA
<213> Conus betulinus
<220>
<221>
      misc feature
      (1)...(226)
<222>
      n may be any nucleotide
<400> 270
ggatccatga tgtctaaact gggagtcttg ttgatcatct gtctgcttct gtttcccctt
                                                                       60
actgctgttc cgctggatgg agatcagcct gcagagcgta cgcagatcga gcagcatccc
                                                                      120
ttgtttgacc agaaaagaag gtgttgccgg tggccatgcc ccagtagatg cggcatggct
                                                                      180
aggtgttgct tcgtcatgat aacgtgttga tgancgacct ctcnag
                                                                      226
<210>
      271
<211>
       67
<212>
      PRT
<213> Conus betulinus
<400> 271
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Phe
Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Glu Arg Thr
            20
                                                     30
Gln Ile Glu Gln His Pro Leu Phe Asp Gln Lys Arg Arg Cys Cys Arg
Trp Pro Cys Pro Ser Arg Cys Gly Met Ala Arg Cys Cys Phe Val Met
    50
Ile Thr Cys
<210>
      272
<211>
       23
<212>
      PRT
<213>
      Conus betulinus
<220>
<221>
       PEPTIDE
<222>
       (1)..(23)
      Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or
       bromo-Trp
<400> 272
```

Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Arg Cys Gly Met Ala Arg Cys Cys Phe Val Met Ile Thr Cys <210> 273 <211> 262 <212> DNA <213> Conus parius <400> 273 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60 actgctcttc cgatggatgg tgatcaacct gcagaccgac ttgtagagcg tatgcaggac 120 aacatttcat ctgagcagca tcccttcttt gaaaagagaa gaggaggctg ttgcacacct 180 ccgaagaaat gcaaagaccg agcctgcaaa cctgcacgtt gctgcggccc aggataacgt 240 gttgatgacc aactttctcg cc 262 274 <210> <211> 76 <212> PRT <213> Conus parius <400> 274 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly <210> 275 <211> 24 <212> PRT <213> Conus parius <220> <221> PEPTIDE <222> (1)...(24)Xaa at residue 7, 8, 18 and 24 is Pro or Hyp <223> <400> 275 Arg Gly Gly Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Ala Cys Lys Xaa Ala Arg Cys Cys Gly Xaa <210> 276 <211> 259 <212> DNA

<213>

Conus parius

```
<400> 276
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt
                                                                       60
actgctcttc cgatggatgg tgatcaacct gcagaccgac ttgtagagcg tatgcaggac
                                                                      120
aacatttcat ctgagcagca tcccttcttt gaaaagagaa gaggctgttg cacacctccg
                                                                      180
aggaaatgca aagaccgagc ctgcaaacct gcacgttgtt gcggcccagg ataacgtgtt
                                                                      240
gatgaccaac tttctcgag
                                                                      259
       277
<210>
<211>
       75
<212>
      PRT
     Conus parius
<213>
<400> 277
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
Glu Lys Arg Arg Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg
Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
<210>
       278
<211>
       23
<212>
      PRT
<213>
      Conus parius
<220>
<221>
      PEPTIDE
<222>
       (1)..(23)
      Xaa at residue 6, 7, 17 and 23 is Pro or Hyp
<400> 278
Arg Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys Lys
                                    10
Xaa Ala Arg Cys Cys Gly Xaa
<210>
       279
<211>
       241
<212>
      DNA
<213>
      Conus coronatus
<400> 279
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccaatt
                                                                       60
                                                                      120
actgcccttc cgctggatga agatcaacct gcagaccgac ctgcagagcg tatgcaggac
attgcaactg aacagcatcc cttgtttgat cccgtcaaac ggtgctgcga ttggccatgc
                                                                      180
atcccaggat gcaccccttg ttgcttgcct tgataacgtg ttgatgacca actttctcga
                                                                      240
g
                                                                      241
```

```
<210>
      280
<211>
       68
<212>
      PRT
<213> Conus coronatus
<400> 280
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Ile Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
            20
Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp
Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ile Pro Gly Cys Thr Pro
    50
                        55
Cys Cys Leu Pro
<210>
      281
<211>
      16
<212>
      PRT
<213> Conus coronatus
<220>
<221> PEPTIDE
<222>
      (1)..(16)
     Xaa at residue 5, 8, 12 and 16 is Pro or Hyp; Xaa at residue 4 is
       Trp or bromo-Trp
<400> 281
Cys Cys Asp Xaa Xaa Cys Ile Xaa Gly Cys Thr Xaa Cys Cys Leu Xaa
                                    10
<210>
      282
      244
<211>
<212>
      DNA
<213> Conus musicus
<400> 282
ggatccatga tgtctaaact gggagtcctg ttgaccatct gtctgcttct gtttcctctt
                                                                      60
tctgctcttc cgatggatga agatcaactt gcagacctac ctgcagagcg tatgcgggac
                                                                     120
actgcaactg tagatcatcc ctcctatgat cctgacaaag cgtgctgcga gcagagctgt
                                                                     180
acaacatgct ttccgtgctg ctagccttga acacagtaac gtgttgatga ccaactttct
                                                                     240
cgag
                                                                     244
<210>
      283
<211>
       65
<212>
      PRT
<213>
      Conus musicus
<400> 283
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Ser Ala Leu Pro Met Asp Glu Asp Gln Leu Ala Asp Leu Pro
```

Ala Glu Arg Met Arg Asp Thr Ala Thr Val Asp His Pro Ser Tyr Asp

35 40 45 Pro Asp Lys Ala Cys Cys Glu Gln Ser Cys Thr Thr Cys Phe Pro Cys 55 Cys 65 <210> 284 <211> 14 <212> PRT <213> Conus musicus <220> <221> PEPTIDE <222> (1)..(14)Xaa at residue4 is Glu or gamma-carboxy Glu; Xaa at residue 12 i <223> s Pro or Hyp <400> 284 Ala Cys Cys Xaa Gln Ser Cys Thr Thr Cys Phe Xaa Cys Cys <210> 285 <211> 14 <212> PRT <213> Conus betulinus <220> <221> PEPTIDE <222> (1)..(14)<223> Xaa at residue 4 is Glu or gamma-carboxy Glu; Xaa at residue 12 i s Pro or Hyp <400> 285 Ala Cys Cys Xaa Gln Ser Cys Thr Thr Cys Met Xaa Cys Cys 10 <210> 286 <211> 14 PRT <212> <213> Conus betulinus <220> <221> PEPTIDE <222> (1)...(14)<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 11 i s Pro or Hyp; Xaa at residue 14 is Trp or bromo-Trp <400> 286 Cys Cys Xaa Gln Ser Cys Thr Thr Cys Met Xaa Cys Cys Xaa <210> 287 <211> 235 <212> DNA <213> Conus pennaceus <400> 287 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60 actgctcttc cgctggatgg agatcaacct gcataccaag ctgcagagcg tatgcaggcc 120 gagcatcatc ccttgtttga tcagaaaaga cggtgctgca agtttccatg ccccgatagt 180

tgcaaatatt tgtgttgcgg gtgatgataa catgttgatg accaactttc ttgag

```
<210>
      288
<211>
       65
      PRT
<212>
<213>
      Conus pennaceus
<400> 288
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Tyr Gln Ala
Ala Glu Arg Met Gln Ala Glu His His Pro Leu Phe Asp Gln Lys Arg
Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Lys Tyr Leu Cys Cys
Gly
65
<210>
      289
<211>
      16
<212>
      PRT
      Conus pennaceus
<220>
<221>
      PEPTIDE
<222>
      (1)..(16)
      Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 13 is Tyr, 1
       25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400> 289
Arg Cys Cys Lys Phe Xaa Cys Xaa Asp Ser Cys Lys Xaa Leu Cys Cys
                                    10
<210> 290
<211>
      241
<212>
      DNA
<213> Conus pulicarius
<400> 290
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt
                                                                      60
actgctcttc cgatggatgg tgatcaactt gcagaccgac ttgtagagcg tatgcaggac
                                                                     120
aacatttcat ctgagcagca tcccttcttt gatcccgtca aacggtgttg cgtcagctgt
                                                                     180
tacatgggat gcatccettg ttgcttctag taataacgtg ttgatgacca actttctcga
                                                                     240
                                                                     241
<210> 291
<211>
       67
<212>
      PRT
<213> Conus pulicarius
<400> 291
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Asp Arg Leu
```

25

```
Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
Asp Pro Val Lys Arg Cys Cys Val Ser Cys Tyr Met Gly Cys Ile Pro
Cys Cys Phe
<210>
       292
<211>
      14
<212>
      PRT
<213> Conus pulicarius
<220>
<221>
       PEPTIDE
<222>
       (1)..(14)
       Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Ty
       r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400> 292
Cys Cys Val Ser Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
<210>
<211>
       244
<212>
       DNA
<213>
     Conus pulicarius
<400> 293
ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtgtcccctt
                                                                       60
actgctcttc cactggatga agatcaactt gcagaccgac ctgcagagcg tatgcaggat
                                                                      120
gacacttcag ctgcacagat tttcgggttt gatcccgtca aacggtgctg caaattgcta
                                                                      180
tgctactcgg gatgcactcc ttgttgccat atttgataac gtgttgatga ccaactttct
                                                                      240
cgag
                                                                      244
<210>
       294
<211>
       67
<212>
       PRT
<213> Conus pulicarius
<400> 294
Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu Cys
Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Leu Ala Asp Arg Pro
Ala Glu Arg Met Gln Asp Asp Thr Ser Ala Ala Gln Ile Phe Gly Phe
Asp Pro Val Lys Arg Cys Cys Lys Leu Cys Gly Cys Thr Pro Cys 50 55 60
Cys His Ile
<210>
       295
<211>
       16
<212>
       PRT
<213> Conus pulicarius
```

```
<220>
<221>
       PEPTIDE
<222>
       (1)..(16)
       Xaa at residue 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Ty
       r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400> 295
Cys Cys Lys Leu Leu Cys Xaa Ser Gly Cys Thr Xaa Cys Cys His Ile
<210>
       296
<211>
       259
<212>
       DNA
<213> Conus rattus
<400> 296
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttgt gtttccgctt
                                                                       60
actqctcttc cqatqqatqq tqatcaacct qcaqaccqac ttqtaqaqcq tatacaqqac
                                                                      120
aacatttcat ctgagcagca tcccttcttt gaaaagagaa gaggctgttg cgcacctccg
                                                                      180
aggaaatgca aagaccgagc ctgcaaacct gcacgttgct gcggcccagg ataacgtgtt
                                                                      240
                                                                      259
gatgaccaac tttctcgag
<210>
       297
<211>
       75
<212>
       PRT
<213>
      Conus rattus
<400> 297
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Val Phe
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
Val Glu Arg Ile Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
                             40
Glu Lys Arg Arg Gly Cys Cys Ala Pro Pro Arg Lys Cys Lys Asp Arg
Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
<210>
       298
<211>
       23
<212>
       PRT
<213>
       Conus rattus
<220>
<221>
       PEPTIDE
<222>
       (1)..(23)
<223>
       Xaa at residue 6, 7, 17 and 23 is Pro or Hyp
<400> 298
Arg Gly Cys Cys Ala Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys Lys
Xaa Ala Arg Cys Cys Gly Xaa
```

```
299
<210>
<211>
       262
<212>
       DNA
<213>
      Conus stercusmuscarum
<400> 299
ggatccatga tgtctaaact gggagtcttg ttgacaatct gtctgcttct gtttcccctt
                                                                       60
attgctcttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac
                                                                      120
gacatttcat ctgagaagca tcccttgttt gataagagac aacggtgttg caatgggcgg
                                                                      180
aggggatgct ccagcagatg gtgcagagat cactcacgtt gttgcggtcg acgataacgt
                                                                      240
gttgatgacc aactttctcg ag
                                                                      262
       300
<210>
<211>
       76
<212>
       PRT
<213>
      Conus stercusmuscarum
<400> 300
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Ile Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Lys His Pro Leu Phe
Asp Lys Arg Gln Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg
Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
<210>
      301
<211>
       22
<212>
      PRT
<213>
      Conus stercusmuscarum
<220>
<221>
      PEPTIDE
<222>
       (1)..(22)
<223>
      Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 14 is Trp or
       bromo-Trp
<400>
       301
Xaa Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg Xaa Cys Arg
Asp His Ser Arg Cys Cys
            20
<210>
       302
<211>
       241
<212>
       DNA
<213> Conus ebraceus
<400> 302
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt
                                                                       60
actgctcttc cactggatga aggtcaacct gcagacctac ctgcagagcg tatgcaggac
                                                                      120
```

```
attgcaactg aacagcatcc cttgtttgat cctgtcaaac ggtgttgcga gcagccatgc
                                                                      180
tacatgggat gcatcccttg ttgcttctaa taataacgtg ttgatgacca actttctcga
                                                                      240
                                                                      241
<210>
       303
<211>
       67
<212>
       PRT
<213>
      Conus ebraceus
<400>
       303
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Leu Asp Glu Gly Gln Pro Ala Asp Leu Pro
            20
Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp
                            40
Pro Val Lys Arg Cys Cys Glu Gln Pro Cys Tyr Met Gly Cys Ile Pro
Cys Cys Phe
<210>
       304
<211>
       15
      PRT
<212>
<213>
      Conus ebraceus
<220>
<221>
       PEPTIDE
<222>
       (1)..(15)
<223>
       Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5 an
       d 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-
       Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400> 304
Cys Cys Xaa Gln Xaa Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
                                    10
<210>
       305
<211>
       241
<212>
       DNA
<213>
       Conus ebraceus
<400>
       305
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt
                                                                       60
actgctcttc cactggatga agatcaacct gcagacctac ctgcagagcg tatgcaggac
                                                                      120
attgcaactg aacagcatcc cttgtttgat cctgtcaaac ggtgctgcgc gcagccatgc
                                                                      180
tacatgggat gcatcccttg ttgcttctaa taataacgtg ttgatgacca actttctcga
                                                                      240
                                                                      241
g
<210>
       306
<211>
       67
<212>
       PRT
<213>
      Conus ebraceus
<400>
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
```

```
1
                                     10
                                                         15
Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Leu Pro
            20
Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp
Pro Val Lys Arg Cys Cys Ala Gln Pro Cys Tyr Met Gly Cys Ile Pro
Cys Cys Phe
65
<210>
       307
<211>
       15
<212>
       PRT
<213>
       Conus ebraceus
<220>
<221>
      PEPTIDE
<222>
       (1)..(15)
       Xaa at residue 5 and 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 1
       251-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
<400>
       307
Cys Cys Ala Gln Xaa Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
<210>
       308
<211>
       238
<212>
       DNA
<213>
      Conus flavidus
<400> 308
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt
                                                                       60
actgctgttc cgttggatgg agatcaacct gcagaccagc ctgcagagcg tatgcagaac
                                                                      120
gagcagcatc ccttgtttga tcagaaaaga aggtgctgcc ggtggccatg ccccagtata
                                                                      180
tgcggcatgg ctaggtgttg ctcgtcatga taacgtgttg atgaccaact ttctcgag
                                                                    - 238
<210>
       309
<211>
       67
<212>
       PRT
      Conus flavidus
<213>
<400> 309
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
Ala Glu Arg Met Gln Asn Glu Gln His Pro Leu Phe Asp Gln Lys Arg
Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
Cys Ser Ser
```

```
<210>
       310
<211>
       19
<212>
       PRT
<213> Conus flavidus
<220>
<221>
       PEPTIDE
<222>
       (1)..(19)
       Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or
       bromo-Trp
<400> 310
Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Ile Cys Gly Met Ala Arg Cys
Cys Ser Ser
<210>
       311
<211>
       245
<212>
      DNA
<213> Conus miliaris
<220>
<221>
      misc_feature
<222>
      (1)...(245)
<223>
      n may be any nucleotide
<400> 311
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccaatt
                                                                       60
actgcccttc cactggatga agatcaacct gcagaccgac ctgcagagcg tatgcaggac
                                                                      120
attgcaactg aacagcatcc cttgtttgat cccgtcaaac ggtgttgcga ttggccatgc
                                                                      180
agegeaggat getaccettg ttgetteeet taataaegtg ttgatgacca aetnangnaa
                                                                      240
                                                                      245
aaaaa
<210> 312
<211>
      68
      PRT
<212>
<213> Conus miliaris
<400> 312
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Ile Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
            20
Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp
Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ser Ala Gly Cys Tyr Pro
Cys Cys Phe Pro
65
<210>
       313
<211>
       16
<212>
       PRT
<213> Conus miliaris
<220>
```

```
<221>
      PEPTIDE
<222>
       (1)..(16)
       Xaa at residue 5, 12 and 16 is Pro or Hyp; Xaa at residue 4 is Tr p or bromo-Trp; Xaa at residue 11 is Tyr, 125I-Tyr, mono-iodo-Tyr
<223>
       , di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400> 313
Cys Cys Asp Xaa Xaa Cys Ser Ala Gly Cys Xaa Xaa Cys Cys Phe Xaa
                                       10
<210>
       314
<211>
      230
<212>
      DNA
<213> Conus miliaris
<220>
       misc_feature
<221>
       (1)...(230)
<222>
<223>
       n may be any nucleotide
<400> 314
ggatccatga tgtctaaact gggagtggtg ccattcgtct ttctggtcct gtttcccctg
                                                                           60
gcaacactcc aactggatgc agatcaacct gcagaccgac ctgcgcgtaa aaagggcatt
                                                                          120
gcaactaaac ggcatccctt gtctgatcct gtcagagggt gttgccctcc aatgtgcaca
                                                                          180
ccatgcttcc cttgctgttt tcgttaataa cgtgttgatg natgatgnan
                                                                          230
<210>
       315
<211>
       66
<212>
       PRT
<213>
       Conus miliaris
<400> 315
Met Met Ser Lys Leu Gly Val Val Pro Phe Val Phe Leu Val Leu Phe
Pro Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Ala Asp Arg Pro
Ala Arg Lys Lys Gly Ile Ala Thr Lys Arg His Pro Leu Ser Asp Pro
Val Arg Gly Cys Cys Pro Pro Met Cys Thr Pro Cys Phe Pro Cys Cys
    50
Phe Arg
65
<210>
       316
<211>
       16
<212>
       PRT
<213>
       Conus miliaris
<220>
<221>
       PEPTIDE
<222>
       (1)..(16)
<223>
       Xaa at residue 4, 9 and 12 is Pro or Hyp; Xaa at residue 5 is Tyr
       , 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
       -Tyr
<400> 316
Gly Cys Cys Xaa Xaa Met Cys Thr Xaa Cys Phe Xaa Cys Cys Phe Arq
                                      10
```

```
<210>
       317
       295
<211>
<212>
       DNA
<213>
       Conus ammiralis
<400> 317
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                       60
gettetgttt cecettactg etetteeget ggatggagat caacetgeag accaagetge
                                                                      120
agagegtatg caggeegage ageateeett gtttgateag aaaagaeggt gttgeaggtt
                                                                      180
tccatgcccc gatacttgca gacatttgtg ttgcgggtga tgataacgtg ctgatgaccc
                                                                      240
actttgtcat cacggctacg tcaagtgtct aatgaataag taaaatgatt gcagt
                                                                      295
<210>
       318
<211>
       65
<212>
       PRT
<213>
      Conus ammiralis
<400> 318
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Ala
            20
Ala Glu Arg Met Gln Ala Glu Gln His Pro Leu Phe Asp Gln Lys Arg
Arg Cys Cys Arg Phe Pro Cys Pro Asp Thr Cys Arg His Leu Cys Cys
Gly
65
<210>
       319
<211>
       16
<212>
       PRT
<213>
      Conus ammiralis
<220>
      PEPTIDE
<221>
<222>
       (1)...(16)
      Xaa at residue 6 and 8 is Pro or Hyp
<400> 319
Arg Cys Cys Arg Phe Xaa Cys Xaa Asp Thr Cys Arg His Leu Cys Cys
                                     10
<210>
       320
<211>
       267
<212>
       DNA
<213>
       Conus ammiralis
<400> 320
caagagggat cgatagcagt tcatgatgtt taaactggga gtcttgctga ccatctgtct
                                                                        60
acttetgttt teeettaatg etgtteeget ggatggagat caacetgeag aceaacetge
                                                                       120
agagegtetg etggaegaea ttteatetga aaataateee ttttatgate eegeeaaaeg
                                                                       180
gtgttgcatg acttgcttcg gttgcacacc ttgttgtgga tgaccagcct catcaagtgt
```

```
ctaacgaata agtaaaacga ttgcagt
                                                                      267
<210>
       321
<211>
       66
       PRT
<212>
<213>
       Conus ammiralis
<400> 321
Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
                                    10
Ser Leu Asn Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
Ala Glu Arg Leu Leu Asp Asp Ile Ser Ser Glu Asn Asn Pro Phe Tyr
Asp Pro Ala Lys Arg Cys Cys Met Thr Cys Phe Gly Cys Thr Pro Cys
                        55
Cys Gly
<210>
      322
<211>
       12
<212> PRT
<213> Conus ammiralis
<220>
      PEPTIDE
<221>
<222>
       (1)..(12)
      Xaa at residue 10 is Pro or Hyp
<400> 322
Cys Cys Met Thr Cys Phe Gly Cys Thr Xaa Cys Cys
<210> 323
<211>
       294
<212>
       DNA
<213>
       Conus ammiralis
<400> 323
caagaaggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct
                                                                       60
acttetgttt teeettaetg etgtteeget ggatggagat caacatgeag accaacetge
                                                                      120
agagegtetg caggacegee ttecaactga aaatcateee ttatatgate cegteaaacg
                                                                     180
gtgttgcgat gattcggaat gcgactattc ttgctggcct tgctgtattt tttcataacc
                                                                     240
tttgttatcg cggcctcatc ctagtgtcaa atgaataagt aaaacgattg cagt
                                                                     294
<210>
       324
<211>
       71
<212>
       PRT
<213> Conus ammiralis
<400> 324
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Phe
Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
            20
                                25
```

Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Ile Phe Ser <210> 325 <211> 18 <212> PRT <213> Conus ammiralis <220> <221> PEPTIDE <222> (1)..(18)Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 i <223> s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at resid ue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o r O-phospho-Tyr <400> 325 Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile Phe Ser <210> 326 <211> 284 <212> DNA <213> Conus ammiralis <400> 326 caagagggat cgatagcagt tcatgatgtt taaactcgga gtcttgctga ccatctgtct 60 acttetgttt teectaattg etgtteeget ggatggagat caacatgeag accaacetge 120 agagegtetg caggacegee ttecaactga aaateateee ttatatgate eegteaaacg 180 gtgttgcagg ttgttatgcc tcagttgcaa cccttgttgt ggatgaccag ctttgttatc 240 acggcctcat caagtgtcta atgaataagt aaaacgattg cagt 284 <210> 327 <211> 67 <212> PRT <213> Conus ammiralis <400> 327 Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr Asp Pro Val Lys Arg Cys Cys Arg Leu Leu Cys Leu Ser Cys Asn Pro Cys Cys Gly

```
<210>
       328
<211>
       13
      PRT
<212>
<213>
      Conus ammiralis
<220>
<221>
       PEPTIDE
<222>
       (1)..(13)
<223>
      Xaa at residue 11 is Pro or Hyp
<400>
       328
Cys Cys Arg Leu Cys Leu Ser Cys Asn Xaa Cys Cys
<210>
       329
<211>
       289
<212>
       DNA
<213>
      Conus ammiralis
<400> 329
caagaaggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct
                                                                       60
acttetgttt teeettactg etgtteeget ggatggagat caacatgeag accaacetge
                                                                      120
agagegtetg caggacegea ttecaactga agateateee ttatttgate ecaacaaacg
                                                                      180
gtgttgcgat gattcggaat gcggctattc atgctggcct tgctgttatg gataagcttt
                                                                      240
gttatcgcgg cctcatccag tgtcaacgaa taagtaaaac gattgcagt
                                                                      289
       330
<210>
<211>
       70
<212>
       PRT
<213>
      Conus ammiralis
<400> 330
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Phe
Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
Ala Glu Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe
Asp Pro Asn Lys Arg Cys Cys Asp Asp Ser Glu Cys Gly Tyr Ser Cys
Trp Pro Cys Cys Tyr Gly
<210>
      331
<211>
       16
<212>
      PRT
<213>
      Conus ammiralis
<220>
<221>
       PEPTIDE
<222>
       (1)..(16)
<223>
      Xaa at residue6 is Glu or gamma-carboxy Glu; Xaa at residue 13 i
       s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at resid
       ue 9 and 16 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulph
```

o-Tyr or O-phospho-Tyr

```
<400> 331
Cys Cys Asp Asp Ser Xaa Cys Gly Xaa Ser Cys Xaa Xaa Cys Cys Xaa
                                    10
<210>
       332
<211>
       272
<212>
       DNA
<213>
      Conus spurius
<400> 332
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccatctgtct
                                                                       60
gettetgttt ceaegtaett etetteeget ggatggagat caaectgeag teegatetge
                                                                      120
aaagcgtatg cattcatcta tacagcgtcg tttctttgat cccqtcaaac qqtqttqccc
                                                                      180
tagatgcagc gagtgcaacc cttgttgtgg atgaccagct ttgtcatcgc ggcctcatta
                                                                      240
agtgtctaat gaataagtaa aatgattgca gt
                                                                      272
<210>
       333
<211>
       63
<212>
       PRT
<213>
       Conus spurius
<400> 333
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
                                    10
Pro Arg Thr Ser Leu Pro Leu Asp Gly Asp Gln Pro Ala Val Arg Ser
Ala Lys Arg Met His Ser Ser Ile Gln Arg Arg Phe Phe Asp Pro Val
Lys Arg Cys Cys Pro Arg Cys Ser Glu Cys Asn Pro Cys Cys Gly
<210>
       334
<211>
       12
<212>
      PRT
<213> Conus spurius
<220>
<221>
      PEPTIDE
<222>
       (1)..(12)
      Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 3 an
       d 10 is Pro or Hyp
<400> 334
Cys Cys Xaa Arg Cys Ser Xaa Cys Asn Xaa Cys Cys
<210>
       335
<211>
       293
<212>
       DNA
<213>
      Conus omaria
<400> 335
caagagggat cgatagcagt tcatgatgtc taaactggga gtctcgttga ccatctgtct
                                                                       60
acttctattt tcccttactg ctgttccgct tgatggagat caacatgcag accaacctgc
                                                                      120
agagegtetg cagggegaca ttttatetga aaageateee ttatttaate eegteaaaeg
                                                                      180
```

gtgttgcgat gaggaagaat gcagcagtgc atgctggcct tgttgttggg ggtgatcagc 240 tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaatgattgc agt 293 <210> 336 <211> 70 <212> PRT <213> Conus omaria <400> 336 Met Met Ser Lys Leu Gly Val Ser Leu Thr Ile Cys Leu Leu Phe 10 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro 20 Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe Asn Pro Val Lys Arg Cys Cys Asp Glu Glu Glu Cys Ser Ser Ala Cys Trp Pro Cys Cys Trp Gly <210> 337 <211> 16 <212> PRT <213> Conus omaria <220> <221> PEPTIDE <222> (1)..(16)Xaa at residue 4, 5 and 6 is Glu or gamma-carboxy Glu; Xaa at res idue 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-T rp <400> 337 Cys Cys Asp Xaa Xaa Cys Ser Ser Ala Cys Xaa Xaa Cys Cys Xaa 10 <210> 338 <211> 293 <212> DNA <213> Conus omaria <400> 338 caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga tcatctgtct 60 acttetgtgt ccccttactg ctgttetgga ggatggagat caacetgeag accgaectge 120 agagegtatg caggaegaea ttteaactga geateateee ttttatgate eegteaaacq 180 gtgttgcaag tacgggtgga catgcttgct aggatgcact ccttgtgatt gttgaccagt 240 tttgttatcg cggcctcgtc aagtgtctaa tgaataagta aaacgattgc agt 293 <210> 339 <211> 70 <212> PRT <213> Conus omaria <400> 339 Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Cys 10

Pro Leu Thr Ala Val Leu Glu Asp Gly Asp Gln Pro Ala Asp Arg Pro Ala Glu Arg Met Gln Asp Asp Ile Ser Thr Glu His His Pro Phe Tyr Asp Pro Val Lys Arg Cys Cys Lys Tyr Gly Trp Thr Cys Leu Leu Gly Cys Thr Pro Cys Asp Cys <210> 340 <211> 17 <212> PRT <213> Conus omaria <220> <221> PEPTIDE <222> (1)..(17)Xaa at residue is 14 Pro or Hyp; Xaa at residue 6 is Trp or bromo -Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-T yr, O-sulpho-Tyr or O-phospho-Tyr <400> 340 Cys Cys Lys Xaa Gly Xaa Thr Cys Leu Leu Gly Cys Thr Xaa Cys Asp Cys <210> 341 <211> 290 <212> DNA <213> Conus omaria <400> 341 caagagggat cgatagcagt tcatgatgtc tatactggga gtcttgttga tcatctgtct 60 acttetgtgt cecettactg etgttetgga ggatggagat caacetgeag acegacetge 120 agagegtatg caggaeggea tttcatetga acateatece tttttggate eegteaaacg 180 gtgttgccat ctattggcat gccgctttgg atgctcgcct tgttgttggt gaccagcttt 240 gttatcqcqq cctcatcaaq tqtctaatqa ataaqtaaaa cqattqcaqt 290 <210> 342 <211> 69 <212> PRT <213> Conus omaria <400> 342 Met Met Ser Ile Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Cys Pro Leu Thr Ala Val Leu Glu Asp Gly Asp Gln Pro Ala Asp Arg Pro 20 30 Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu His His Pro Phe Leu Asp Pro Val Lys Arg Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys

```
Ser Pro Cys Cys Trp
<210>
       343
<211>
       16
<212>
      PRT
<213>
      Conus omaria
<220>
<221>
      PEPTIDE
<222>
       (1)..(16)
<223>
      Xaa at residue 13 is Pro or Hyp; Xaa at residue 16 is Trp or brom
       o-Trp
<400> 343
Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Xaa Cys Cys Xaa
<210>
       344
<211>
       293
<212>
      DNA
<213>
      Conus omaria
<400> 344
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga tcatctgtct
                                                                       60
acttetttqt cecettactq etqtteeqea qqatqqaqat caacetqeaq accqaeetqe
                                                                      120
agagegtatg cagggeggea tttcatetga acateateee ttttttgate eegteaaaeg
                                                                      180
gtgttgcagg tacgggtgga catgctggct aggatgcact ccctgtggtt gttgaccagc
                                                                      240
tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt
                                                                      293
<210>
       345
<211>
       70
<212>
      PRT
<213> Conus omaria
<400> 345
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Cys
Pro Leu Thr Ala Val Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
            20
Ala Glu Arg Met Gln Gly Gly Ile Ser Ser Glu His His Pro Phe Phe
Asp Pro Val Lys Arg Cys Cys Arg Tyr Gly Trp Thr Cys Trp Leu Gly
    50
Cys Thr Pro Cys Gly Cys
<210>
       346
<211>
       17
<212>
       PRT
<213> Conus omaria
<220>
<221>
       PEPTIDE
<222>
       (1)..(17)
      Xaa at residue 14 is Pro or Hyp; Xaa at residue 6 and 9 is Trp or
        bromo-Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
```

99 iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr <400> 346 Cys Cys Arg Xaa Gly Xaa Thr Cys Xaa Leu Gly Cys Thr Xaa Cys Gly 10 Cys <210> 347 <211> 293 <212> DNA <213> Conus episcopatus <400> 347 caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60 acttctgttt tcccttattg ctgttccgct tgatggagat caacatgcag accaacctgc 120 agagegtetg cagggegaca ttttatetga aaageateee ttatttatge etgteaaaeg 180 gtgttgcgat gaggacgaat gcaacagttc atgctggcct tgttgttggg ggtgatcagc 240 tttgttatcg cggcctgatc aagtgtataa tgaataagta aaacgattgc agt 293 <210> 348 <211> 70 <212> PRT <213> Conus episcopatus <400> 348 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe Met Pro Val Lys Arg Cys Cys Asp Glu Asp Glu Cys Asn Ser Ser Cys Trp Pro Cys Cys Trp Gly <210> 349 <211> 16 <212> PRT <213> Conus episcopatus

```
Xaa at residue 4 and 6 is Glu or gamma-carboxy Glu; Xaa at residu
<223>
       e 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-Trp
<400>
       349
Cys Cys Asp Xaa Asp Xaa Cys Asn Ser Ser Cys Xaa Xaa Cys Cys Xaa
                                     10
<210>
       350
<211>
       293
<212>
       DNA
```

<220> <221>

<222>

PEPTIDE

(1)..(16)

```
<213> Conus episcopatus
<400>
       350
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                       60
acttetgttt teeettattg etgtteeget tgatggagat caacatgeag accaacetge
                                                                      120
agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttatgc ctgtcaaacg
                                                                      180
gtqttqcqat gaggacqaat gcagcagttc atgctggcct tgttgttggg gatgagcagc
                                                                      240
tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt
                                                                      293
<210>
       351
<211>
       70
<212>
       PRT
<213>
      Conus episcopatus
<400>
       351
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
Met Pro Val Lys Arg Cys Cys Asp Glu Asp Glu Cys Ser Ser Cys
Trp Pro Cys Cys Trp Gly
<210>
       352
<211>
       16
<212>
      PRT
<213> Conus episcopatus
<220>
       PEPTIDE
<221>
<222>
       (1)..(16)
       Xaa at residue4 and 6 is Glu or gamma-carboxy Glu; Xaa at residu
<223>
       e 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-Trp
<400> 352
Cys Cys Asp Xaa Asp Xaa Cys Ser Ser Ser Cys Xaa Xaa Cys Cys Xaa
<210>
       353
<211>
       290
<212>
       DNA
<213>
       Conus episcopatus
<400> 353
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                       60
acttetgttt teeettactg etgtteeget tgatggagat caacatgeag accaacetge
                                                                      120
agagegtetg cagggegaca ttttatetga aaageateee ttatttaate eegteaaaeg
                                                                      180
gtgttgcccg gcggcggcat gtgccatggg atgcaagcct tgttgtggat gagcagcttt
                                                                      240
gttatcgtgg cctcatcaag tgtctaatga ataagtaaaa cgattgcagt
                                                                      290
```

```
<210>
      354
<211>
       69
<212>
      PRT
<213>
      Conus episcopatus
<400> 354
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
Asn Pro Val Lys Arg Cys Cys Pro Ala Ala Ala Cys Ala Met Gly Cys
Lys Pro Cys Cys Gly
<210> 355
<211>
      15
<212>
      PRT
<213> Conus episcopatus
<220>
<221>
      PEPTIDE
<222>
       (1)..(15)
      Xaa at residue 3 and 13 is Pro or Hyp
<400> 355
Cys Cys Xaa Ala Ala Cys Ala Met Gly Cys Lys Xaa Cys Cys
<210>
      356
<211>
      295
<212>
      DNA
<213> Conus aulicus
<400> 356
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                      60
gettetgttt teegttactg etetteegee ggatggagat caacetgeag acegagetge
                                                                     120
agagegtagg caggtegage ageateeegt gtttgateat gaaagagggt gttgetegee
                                                                     180
accatgccac agtatttgcg ctgctttctg ttgcgggtga tgataacgtg ttgatgaccc
                                                                     240
actttgtcat cacggctgcg tcaagtgtct aatgaataag taaaatgatt gcagt
                                                                     295
<210>
      357
<211>
      65
<212>
      PRT
<213>
     Conus aulicus
<400> 357
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Ser Val Thr Ala Leu Pro Pro Asp Gly Asp Gln Pro Ala Asp Arg Ala
```

Ala Glu Arg Arg Gln Val Glu Gln His Pro Val Phe Asp His Glu Arg

```
35
                             40
                                                 45
Gly Cys Cys Ser Pro Pro Cys His Ser Ile Cys Ala Ala Phe Cys Cys
                        55
                                             60
Gly
65
<210>
       358
<211>
       16
       PRT
<212>
<213>
       Conus aulicus
<220>
       PEPTIDE
<221>
<222>
       (1)..(16)
<223>
      Xaa at residue 5 and 6 is Pro or Hyp
<400>
Gly Cys Cys Ser Xaa Xaa Cys His Ser Ile Cys Ala Ala Phe Cys Cys
                                     10
<210>
       359
<211>
       290
<212>
       DNA
<213>
       Conus aulicus
<400> 359
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                        60
acttctgttt tcccttactg ctgttccgct tgatggagat caacatgcag accaacctgc
                                                                       120
agagegtetg cagggegaca ttttatetga aaageateee ttatttaate eegteaaacg
                                                                       180
gtgttgccga ccggtggcat gtgccatggg atgcaagcct tgttgtggat gagcagcttt
                                                                       240
gttatcgtgg cctcatcaag tgtctaatga ataagtaaaa tgattgcagt
                                                                       290
<210>
       360
<211>
       69
       PRT
<212>
<213>
      Conus aulicus
<400> 360
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
            20
Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
Asn Pro Val Lys Arg Cys Cys Arg Pro Val Ala Cys Ala Met Gly Cys
Lys Pro Cys Cys Gly
65
<210>
       361
<211>
       15
<212>
       PRT
<213>
       Conus aulicus
<220>
```

```
<221>
      PEPTIDE
<222>
       (1)..(15)
      Xaa at residue 4 and 13 is Pro or Hyp
<223>
<400> 361
Cys Cys Arg Xaa Val Ala Cys Ala Met Gly Cys Lys Xaa Cys Cys
<210>
       362
<211>
       290
<212>
       DNA
<213> Conus aulicus
<400> 362
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga tcatctqtct
                                                                       60
actictgict coccitacty cigiticcyct ggatggagat caaccigcag accqaccigc
                                                                      120
agagcgtatg caggacgaca tttcatctga acatcaaccc atgtttgatg ccatcagaca
                                                                      180
gtgttgcccg gcggtggcat gcgccatggg atgcgagcct tgttgtggat gaccagcttt
                                                                      240
gttatcgcgg cctcatcaag tgtctaatga ataagtaaaa tgattgcagt
                                                                      290
<210>
       363
<211>
       69
<212>
       PRT
<213> Conus aulicus
<400> 363
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Ser
Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His Gln Pro Met Phe
Asp Ala Ile Arg Gln Cys Cys Pro Ala Val Ala Cys Ala Met Gly Cys
Glu Pro Cys Cys Gly
65
<210>
       364
<211>
       16
<212>
      PRT
<213> Conus aulicus
<220>
<221>
       PEPTIDE
<222>
       (1)..(16)
       Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 13 is Glu or
       gamma-carboxy Glu; Xaa at residue 4 and 14 is Pro or Hyp
<400>
Xaa Cys Cys Xaa Ala Val Ala Cys Ala Met Gly Cys Xaa Xaa Cys Cys
                                    10
<210>
       365
<211>
       293
<212>
       DNA
<213> Conus aureus
```

```
<400> 365
caagaaggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct
                                                                           60
acttetgttt tecettaetg etgtteeget ggatggagat caacatgeag accaacatge
                                                                          120
agagegtetg catgacegee ttecaactga aaatcateee ttatatgate eegteaaacq
                                                                          180
gtgttgcgat gattcggaat gcgactattc ttgctggcct tgctgtattt ttggataacc
                                                                          240
tttgttatcg cggcctcatc aagtgtcaaa tgaataagta aaacgattgc agt
                                                                          293
<210>
       366
<211>
       71
<212>
       PRT
<213>
       Conus aureus
<400>
       366
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Phe
Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln His
Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
    50
                                               60
Trp Pro Cys Cys Ile Phe Gly
<210>
       367
<211>
       17
       PRT
<212>
<213>
       Conus aureus
<220>
<221>
       PEPTIDE
<222>
       (1)..(17)
       Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 i
       s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o
       r O-phospho-Tyr
<400>
       367
Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile
                                      10
Phe
<210>
       368
<211>
       290
<212>
       DNA
<213>
       Conus aureus
<400>
caagagggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct
                                                                           60
acttetgttt tecetaactg etgtteeget ggatggagat caacatgeag accaacetge
                                                                          120
agagcgtctg caggaccgca ttccaactga aaatcatccc ttatttgatc cgaacaaacg
                                                                          180
gtgttgcaat gattgggaat gcgacgattc atgctggcct tgctgttatg gataaccttt
                                                                          240
```

```
gttatcgcgg cctcatcaag tgtcaaatga ataagtaaaa cgattgcagt
                                                                      290
<210>
       369
       70
<211>
<212>
       PRT
<213>
      Conus aureus
<400> 369
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Phe
Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
Ala Glu Arg Leu Gln Asp Arg Ile Pro Thr Glu Asn His Pro Leu Phe
Asp Pro Asn Lys Arg Cys Cys Asn Asp Trp Glu Cys Asp Asp Ser Cys
Trp Pro Cys Cys Tyr Gly
<210>
       370
<211>
       16
<212>
       PRT
<213> Conus aureus
<220>
<221>
      PEPTIDE
<222>
       (1)..(16)
<223>
       Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 i
       s Pro or Hyp; Xaa at residue 5 and 12 is Trp or bromo-Trp; Xaa a
       t residue 16 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulp
       ho-Tyr or O-phospho-Tyr
<400> 370
Cys Cys Asn Asp Xaa Xaa Cys Asp Asp Ser Cys Xaa Xaa Cys Cys Xaa
<210>
       371
<211>
       310
<212>
       DNA
<213>
      Conus consors
<400>
       371
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgttt
                                                                       60
gettetgttt eccettactg etetteeaat ggatggagat eaatetgtag acegacetge
                                                                      120
agagcgtatg caggacgaca tttcatctga gctgcatccc ttgttcaatc agaaaagaat
                                                                      180
gtgttgcggc gaaggtgcgc catgccccag ctatttcaga aacagtcaga tttgtcattg
                                                                      240
ttgttaaatg acaacgtgtc gatgaccaac ttcgttatca cgactaatga ataagtaaaa
                                                                      300
tgattgcagt
                                                                      310
<210>
       372
<211>
       74
<212>
       PRT
<213>
       Conus consors
<400> 372
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
```

```
1
                                     10
                                                         15
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro
            20
                                25
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Leu His Pro Leu Phe
Asn Gln Lys Arg Met Cys Cys Gly Glu Gly Ala Pro Cys Pro Ser Tyr
Phe Arg Asn Ser Gln Ile Cys His Cys Cys
<210>
       373
<211>
       22
<212>
       PRT
<213>
      Conus consors
<220>
<221>
      PEPTIDE
<222>
       (1)..(22)
<223>
      Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 8 an
       d 10 is Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo
       -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400> 373
Met Cys Cys Gly Xaa Gly Ala Xaa Cys Xaa Ser Xaa Phe Arg Asn Ser
Gln Ile Cys His Cys Cys
            20
<210>
       374
       315
<211>
<212>
       DNA
<213>
       Conus consors
<400> 374
taagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct
                                                                       60
gcttctgttt ccccttattg ctcttccaat ggatggagat caacctgcag accgacctgc
                                                                      120
agagcgtatg caggacgaca tttcatctca gcagcatccc ttgtttgata agagaggccg
                                                                      180
ctgttgcgat gtgccgaacg catgctccgg cagatggtgc agagatcacg cacaatgttg
                                                                       240
cggatgacga taacgtgttg atgaccaact ttgtgatcac ggctacatca agtgaataag
                                                                      300
taaaacgatt gcagt
                                                                       315
<210>
       375
<211>
       74
<212>
       PRT
<213> Conus consors
<400> 375
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Ile Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Pro
            20
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Gln Gln His Pro Leu Phe
        35
                            40
                                                 45
```

```
Asp Lys Arg Gly Arg Cys Cys Asp Val Pro Asn Ala Cys Ser Gly Arg
Trp Cys Arg Asp His Ala Gln Cys Cys Gly
<210>
       376
<211>
       22
<212>
       PRT
<213> Conus consors
<220>
<221>
       PEPTIDE
<222>
      (1)..(22)
      Xaa at residue 7 is Pro or Hyp; Xaa at residue 14 is Trp or bromo
       -Trp
<400> 376
Gly Arg Cys Cys Asp Val Xaa Asn Ala Cys Ser Gly Arg Xaa Cys Arg
Asp His Ala Gln Cys Cys
<210>
       377
<211>
       322
<212>
      DNA
<213> Conus consors
<400> 377
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ctgtctgttt
                                                                       60
gettetgttt eccettaetg etetteegat ggatggagat eaacetgeag aceaacetge
                                                                      120
agagcgtatg caggacgaca tttcatctga gcagcatccc ttgtttgata agagacaaaq
                                                                      180
gtgttgcact gggaagaagg ggtcatgctc cggtaaagca tgcaaaagtc tcaaatgttg
                                                                      240
ctctggacga taacgtgttg atgaccaact ttgttatcac ggctacgtca agtgtctagt
                                                                      300
gaataagtaa aacgattgca gt
                                                                      322
<210>
       378
<211>
       76
<212>
      PRT
<213> Conus consors
<400> 378
Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu Phe
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Leu Phe
Asp Lys Arg Gln Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly 50 55 60
Lys Ala Cys Lys Ser Leu Lys Cys Cys Ser Gly Arg
<210> 379
```

```
<211>
       23
<212>
      PRT
<213>
      Conus consors
<220>
       PEPTIDE
<221>
<222>
      (1)..(23)
<223>
      Xaa at residue 1 is Gln or pyro-Glu
<400> 379
Xaa Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
Lys Ser Leu Lys Cys Cys Ser
            20
<210>
       380
<211>
       284
<212>
       DNA
<213>
      Conus emaciatus
<400> 380
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccatctgtct
                                                                       60
gcttctgttt ccccttactg ttcttccgat ggatggagat caacctgcag acctacctgc
                                                                      120
attgcgtgcg cagttctttg cacctgaaca tagtccccgg tttgaccccg tcaaacggtg
                                                                      180
ctgctcgcgg gattgcagtg tttgcatccc ttgttgcccg tatggatcac cttgattatt
                                                                      240
gcggccacgt caagtgtcta atgaataagt aaaatgattg cagt
                                                                      284
<210>
       381
<211>
       70
<212>
      PRT
<213>
      Conus emaciatus
<400> 381
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe
Pro Leu Thr Val Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Leu Pro
            20
Ala Leu Arg Ala Gln Phe Phe Ala Pro Glu His Ser Pro Arg Phe Asp
Pro Val Lys Arg Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Pro Cys
    50
Cys Pro Tyr Gly Ser Pro
<210>
       382
<211>
       18
<212>
       PRT
<213> Conus emaciatus
<220>
<221>
       PEPTIDE
<222>
       (1)..(18)
      Xaa at residue 11, 14 and 18 is Pro or Hyp; Xaa at residue 15 is
       Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos
       pho-Tyr
```

```
<400> 382
Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Xaa Cys Cys Xaa Xaa Gly
                                   10
Ser Xaa
<210> 383
<211>
       13
<212> PRT
<213> Conus aurisiacus
<400> 383
Cys Cys Lys Val Gln Cys Glu Ser Cys Thr Pro Cys Cys
<210>
      384
<211>
      15
<212> PRT
<213> Conus atlanticus
<400> 384
Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe Cys Val Pro Cys Cys
<210> 385
<211> 14
<212> PRT
<213> Conus arentus
<400> 385
Cys Cys Glu Arg Pro Cys Asn Ile Gly Cys Val Pro Cys Cys
<210> 386
<211>
     16
<212> PRT
<213> Conus bandus
<400> 386
Cys Cys Asn Trp Pro Cys Ser Met Gly Cys Ile Pro Cys Cys Tyr Tyr
                                   10
<210>
      387
<211> 15
<212> PRT
<213> Conus betulinus
<400> 387
Cys Cys Glu Leu Pro Cys His Gly Cys Val Pro Cys Cys Trp Pro
<210> 388
<211> 16
<212> PRT
<213> Conus betulinus
<400> 388
Cys Cys Gly Leu Pro Cys Asn Gly Cys Val Pro Cys Cys Trp Pro Ser
                                   10
<210>
       389
<211>
      18
<212>
      PRT
<213> Conus betulinus
```

```
<400> 389
Cys Cys Ser Arg Asn Cys Ala Val Cys Ile Pro Cys Cys Pro Asn Trp
Pro Ala
<210>
       390
<211>
       14
<212> PRT
<213> Conus betulinus
<400> 390
Cys Cys Lys Gln Ser Cys Thr Thr Cys Met Pro Cys Cys Trp
<210>
       391
<211> 14
<212> PRT
<213>
     Conus betulinus
<220>
<221>
      PEPTIDE
<222>
       (1)..(14)
<223>
      Xaa is Glu or gamma-carboxy Glu
<400> 391
Ala Cys Cys Xaa Gln Ser Cys Thr Thr Cys Met Pro Cys Cys
      392
<210>
<211>
       14
<212>
      PRT
<213> Conus betulinus
Cys Cys Glu Gln Ser Cys Thr Thr Cys Met Pro Cys Cys Trp
<210>
      393
<211>
       18
<212> PRT
<213> Conus caracteristicus
<400> 393
Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser Cys His Gly Ser Cys Cys
Tyr Lys
<210> 394
<211> 15
<212> PRT
<213>
      Conus caracteristicus
<400> 394
Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys Lys Pro Cys Cys
                                    10
<210>
       395
<211>
       17
<212>
      PRT
<213>
      Conus caracteristicus
<400> 395
```

```
Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Met
Phe
<210>
       396
<211>
      14
<212> PRT
<213>
     Conus caracteristicus
<400> 396
Cys Cys Arg Arg Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
<210> 397
<211> 16
<212> PRT
<213> Conus textile
<400> 397
Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys Lys Pro Cys Cys Gly
<210> 398
<211> 19
<212> PRT
<213> Conus marmoreus
<220>
<221> PEPTIDE
<222> (1)..(19)
<223> Xaa is Hyp
<400> 398
Ser Lys Gln Cys Cys His Leu Ala Ala Cys Arg Phe Gly Cys Thr Xaa
Cys Cys Asn
<210> 399
<211>
      15
<212> PRT
<213> Conus capitaneus
<400> 399
Ser Cys Cys Arg Asp Cys Gly Glu Asp Cys Val Gly Cys Cys Arg
<210>
      400
<211>
       16
<212>
      PRT
<213>
     Conus coronatus
<400> 400
Cys Cys Asp Trp Pro Cys Ile Pro Gly Cys Thr Pro Cys Cys Leu Pro
                                    10
<210> 401
<211> 18
<212>
     PRT
<213> Conus dalli
<400> 401
Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Ile
```

```
Leu Ser
<210> 402
<211> 17
<212> PRT
<213> Conus dalli
<400> 402
Glx Gln Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys Glu Pro Cys
                                    10
Cys
<210> 403
<211>
      16
<212>
      PRT
<213>
      Conus dalli
<400> 403
Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys Thr Pro Cys Cys Trp
<210>
      404
<211>
      14
<212> PRT
<213> Conus distans
<400> 404
Glx Cys Cys Val His Pro Cys Pro Cys Thr Pro Cys Cys Arg
<210>
      405
<211>
      14
<212>
      PRT
<213>
     Conus figulinus
<400> 405
Cys Cys Pro Trp Pro Cys Asn Ile Gly Cys Val Pro Cys Cys
<210>
      406
<211>
      14
<212> PRT
<213> Conus figulinus
<400> 406
Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Pro Cys Cys Pro
<210>
       407
<211>
      15
<212> PRT
<213> Conus figulinus
<400> 407
Cys Cys Arg Trp Pro Cys Pro Ala Arg Cys Gly Ser Cys Cys Leu
      408
<210>
<211>
      16
<212> PRT
<213> Conus figulinus
<400> 408
Cys Cys Glu Leu Ser Arg Cys Leu Gly Cys Val Pro Cys Cys Thr Ser
```

```
10
                                                        15
<210> 409
<211> 16
<212> PRT
<213> Conus figulinus
<400> 409
Cys Cys Glu Leu Ser Lys Cys His Gly Cys Val Pro Cys Cys Ile Pro
<210>
     410
<211> 16
<212> PRT
<213> Conus generalis
<400> 410
Glx Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Val Pro
<210> 411
<211>
     16
<212> PRT
<213> Conus generalis
<400> 411
Glx Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Leu Thr
                                    10
<210> 412
<211> 16
<212> PRT
<213> Conus generalis
<400> 412
Glx Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Val Pro
<210> 413
<211> 17
<212> PRT
<213> Conus gloriamaris
<400> 413
Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Met
Phe
<210> 414
<211> 17
<212>
     PRT
<213> Conus gloriamaris
<400> 414
Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Pro Cys Cys
                                    10
Trp
<210>
     415
<211> 16
<212> PRT
<213> Conus gloriamaris
```

```
<400> 415
Cys Cys Ser Trp Asp Val Cys Asp His Pro Ser Cys Thr Cys Cys Gly
<210> 416
<211> 13
<212> PRT
<213> Conus laterculatus
<400> 416
Cys Cys Asp Trp Pro Cys Ser Gly Cys Ile Pro Cys Cys
<210> 417
<211> 19
<212> PRT
<213> Conus leopardus
<400> 417
Glx Ile Asn Cys Cys Pro Trp Pro Cys Pro Ser Thr Cys Arg His Gln
Cys Cys His
<210> 418
<211>
       19
<212> PRT
<213> Conus lividus
<400> 418
Glx Ile Asn Cys Cys Pro Trp Pro Cys Pro Asp Ser Cys His Tyr Gln
Cys Cys His
<210> 419
<211> 14
<212> PRT
<213> Conus marmoreus
<400> 419
Cys Cys Arg Leu Ser Cys Gly Leu Gly Cys His Pro Cys Cys
                                    1.0
<210> 420
<211> 17
<212> PRT
<213> Conus marmoreus
<400> 420
Glu Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Pro Cys Cys
Val
<210> 421
<211>
       19
<212> PRT
<213> Conus marmoreus
<400> 421
Ser Lys Gln Cys Cys His Leu Pro Ala Cys Arg Phe Gly Cys Thr Pro
Cys Cys Trp
```

```
<210> 422
<211>
      17
<212> PRT
<213> Conus marmoreus
<400> 422
Met Gly Cys Cys Pro Phe Pro Cys Lys Thr Ser Cys Thr Thr Leu Cys
Cys
<210> 423
<211> 14
<212> PRT
<213> Conus musicus
<400> 423
Ala Cys Cys Glu Gln Ser Cys Thr Thr Cys Phe Pro Cys Cys
                                   10
<210> 424
<211> 15
<212> PRT
<213> Conus nobilis
<400> 424
Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe Cys Val Pro Cys Cys
<210> 425
<211> 14
<212> PRT
<213> Conus pulicarius
<400> 425
Cys Cys Asn Ser Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
<210> 426
<211>
      17
<212>
      PRT
<213> Conus quercinus
<400> 426
Glx Arg Cys Cys Gln Trp Pro Cys Pro Gly Ser Cys Arg Cys Cys Arg
Thr
<210>
      427
<211>
      18
<212> PRT
<213> Conus quercinus
<400> 427
Glx Arg Cys Cys Arg Trp Pro Cys Pro Gly Ser Cys Arg Cys Cys Arg
                                   10
Tyr Arg
<210> 428
<211> 18
<212>
      PRT
<213> Conus quercinus
```

```
<400> 428
Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser Cys His Gly Ser Cys Cys
Tyr Lys
<210> 429
<211> 15
<212> PRT
<213> Conus quercinus
<220>
<221>
     PEPTIDE
<222>
      (1)..(15)
<223> Xaa is Hyp
<400> 429
Cys Cys Ser Gln Asp Cys Leu Val Cys Ile Xaa Cys Cys Pro Asn
                                    10
<210> 430
<211> 15
<212> PRT
<213> Conus quercinus
<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa is Hyp
<400> 430
Cys Cys Ser Arg His Cys Trp Val Cys Ile Xaa Cys Cys Pro Asn
<210>
      431
<211>
      16
<212>
     PRT
<213> Conus rattus
<400> 431
Glx Thr Cys Cys Ser Asn Cys Gly Glu Asp Cys Asp Gly Cys Cys Gln
                                    10
<210> 432
<211> 20
<212> PRT
<213> Conus striatus
<400> 432
Glx Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys Trp Cys Arg Asp His
                                    10
Ala Arg Cys Cys
<210>
      433
<211>
       12
      PRT
<212>
<213> Conus textile
<220>
<221> PEPTIDE
<222>
      (1)..(12)
<223> Xaa is Hyp
```

```
<400> 433
Cys Cys Arg Thr Cys Phe Gly Cys Thr Xaa Cys Cys
<210> 434
<211>
      14
      PRT
<212>
<213> Conus tessulatus
<400> 434
Cys Cys His Lys Cys Tyr Met Gly Cys Ile Pro Cys Cys Ile
<210>
      435
<211>
      18
<212>
      PRT
<213>
     Conus tessulatus
<400> 435
Lys Cys Cys Arg Pro Pro Cys Ala Met Ser Cys Gly Met Ala Arg Cys
Cys Tyr
<210> 436
<211>
      23
<212> PRT
<213> Conus betulinus
<400> 436
Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
Cys Phe Val Met Ile Thr Cys
<210> 437
<211>
      23
<212>
      PRT
<213> Conus betulinus
<400> 437
Arg Cys Cys Arg Trp Pro Cys Pro Ser Arg Cys Gly Met Ala Arg Cys
Cys Phe Val Met Ile Thr Cys
<210>
       438
<211>
      15
<212>
     PRT
<213> Conus textile
<400> 438
Phe Cys Cys Asp Ser Asn Trp Cys His Asp Cys Glu Cys Cys Tyr
                                    10
<210>
      439
<211>
      16
<212>
      PRT
<213> Conus marmoreus
<400> 439
Cys Cys His Trp Asn Trp Cys Asp His Leu Cys Ser Cys Cys Gly Ser
```

```
10
                                                        15
<210>
      440
<211>
      16
<212>
      PRT
<213> Conus marmoreus
<220>
<221>
      PEPTIDE
<222>
      (1)..(16)
<223> Xaa is Hyp
<400> 440
Asp Cys Cys Xaa Leu Pro Ala Cys Pro Phe Gly Cys Asn Xaa Cys Cys
<210>
      441
<211>
      16
<212>
      PRT
<213>
      Conus marmoreus
<220>
<221> PEPTIDE
<222>
      (1)..(16)
<223> Xaa is Hyp
<400> 441
Cys Cys Ala Pro Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
                                    10
<210> 442
<211> 16
<212> PRT
<213> Conus marmoreus
<220>
<221>
      PEPTIDE
<222>
      (1)..(16)
<223> Xaa is Hyp
<400> 442
Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
                                    10
<210> 443
<211> 16
<212> PRT
<213> Conus marmoreus
<400> 443
Cys Cys Ala Pro Ser Ala Cys Arg Leu Gly Cys Arg Pro Cys Cys Arg
                                    10
<210> 444
<211> 17
<212> PRT
<213> Conus marmoreus
<220>
<221>
      PEPTIDE
<222>
      (1)..(17)
<223> Xaa is Hyp.
<400> 444
Gly Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys
```

```
10
                                                        15
Val
<210> 445
<211> 15
<212> PRT
<213> Conus textile
<400> 445
Cys Cys Ser Trp Asp Val Cys Asp His Pro Ser Cys Thr Cys Cys
                                    10
<210>
      446
<211> 16
<212> PRT
<213> Conus textile
<400> 446
Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Arg Tyr Leu Cys Cys
                                    10
<210> 447
<211>
      17
<212>
      PRT
<213> Conus aureus
<400> 447
Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Ile
                                    10
Phe
<210>
       448
<211>
      16
<212>
     PRT
<213>
     Conus aureus
<400> 448
Cys Cys Asn Asp Trp Glu Cys Asp Asp Ser Cys Trp Pro Cys Cys Tyr
                                    10
<210> 449
<211> 16
<212> PRT
<213> Conus ammiralis
<400> 449
Arg Cys Cys Arg Phe Pro Cys Pro Asp Thr Cys Arg His Leu Cys Cys
                                    10
<210> 450
<211> 12
<212> PRT
<213> Conus ammiralis
<400> 450
Cys Cys Met Thr Cys Phe Gly Cys Thr Pro Cys Cys
<210>
      451
<211>
       18
<212>
       PRT
<213> Conus ammiralis
```

```
<400> 451
Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Ile
Phe Ser
<210> 452
<211> 13
<212> PRT
<213> Conus ammiralis
<400> 452
Cys Cys Arg Leu Cys Leu Ser Cys Asn Pro Cys Cys
<210> 453
<211> 16
<212> PRT
<213> Conus ammiralis
<400> 453
Cys Cys Asp Asp Ser Glu Cys Gly Tyr Ser Cys Trp Pro Cys Cys Tyr
                                    10
<210> 454
<211> 16
<212> PRT
<213> Conus aulicus
<400> 454
Gly Cys Cys Ser Pro Pro Cys His Ser Ile Cys Ala Ala Phe Cys Cys
                                    10
<210> 455
<211> 15
<212> PRT
<213> Conus aulicus
<400> 455
Cys Cys Arg Pro Val Ala Cys Ala Met Gly Cys Lys Pro Cys Cys
                                    10
<210> 456
<211>
      16
<212> PRT
<213> Conus aulicus
<400> 456
Glx Cys Cys Pro Ala Val Ala Cys Ala Met Gly Cys Glu Pro Cys Cys
                                    10
<210> 457
<211>
      18
<212>
     PRT
     Conus emaciatus
<400> 457
Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Pro Cys Cys Pro Tyr Gly
Ser Pro
<210> 458
<211> 16
<212>
      PRT
<213> Conus episcopatus
```

```
<400> 458
Cys Cys Asp Glu Asp Glu Cys Asn Ser Ser Cys Trp Pro Cys Cys Trp
<210>
       459
<211>
       16
<212>
      PRT
<213>
      Conus episcopatus
<400> 459
Cys Cys Asp Glu Asp Glu Cys Ser Ser Ser Cys Trp Pro Cys Cys Trp
                                    10
<210>
<211>
<212>
      PRT
<213> Conus episcopatus
<400> 460
Cys Cys Pro Ala Ala Ala Cys Ala Met Gly Cys Lys Pro Cys Cys
<210>
      461
<211>
       16
<212>
       PRT
<213>
      Conus omaria
<400> 461
Cys Cys Asp Glu Glu Cys Ser Ser Ala Cys Trp Pro Cys Cys Trp
                                    10
<210>
      462
<211>
       16
<212>
       PRT
      Conus omaria
<213>
<400> 462
Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Pro Cys Cys Trp
<210>
      463
<211>
       12
<212>
       PRT
<213> Conus spurius
<400> 463
Cys Cys Pro Arg Cys Ser Glu Cys Asn Pro Cys Cys
<210>
       464
<211>
       16
<212>
      PRT
<213>
      Conus pennaceus
<400> 464
Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Lys Tyr Leu Cys Cys
<210>
       465
<211>
      19
<212>
      PRT
<213> Conus flavidus
<400> 465
Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
```

```
10
                                                        15
Cys Ser Ser
<210> 466
<211> 14
<212> PRT
<213> Conus pulicarius
<400> 466
Cys Cys Lys Leu Cys Gly Cys Thr Pro Cys Cys His Ile
                                    10
<210> 467
<211> 15
<212> PRT
<213> Conus ebraceus
<400> 467
Cys Cys Glu Gln Pro Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
                                    10
<210> 468
<211> 15
<212> PRT
<213> Conus ebraceus
<400> 468
Cys Cys Ala Gln Pro Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
                                    10
<210> 469
<211> 14
<212> PRT
<213> Conus pulicarius
<400> 469
Cys Cys Val Ser Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
<210> 470
<211>
      16
<212> PRT
<213> Conus miliaris
<400> 470
Cys Cys Asp Trp Pro Cys Ser Ala Gly Cys Tyr Pro Cys Cys Phe Pro
                                    10
<210>
      471
<211>
      16
<212>
     PRT
<213> Conus miliaris
<400> 471
Gly Cys Cys Pro Pro Met Cys Thr Pro Cys Phe Pro Cys Cys Phe Arg
                                    10
<210> 472
<211> 23
<212>
     PRT
<213> Conus rattus
<400> 472
Arg Gly Cys Cys Ala Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys Lys
```

```
Pro Ala Arg Cys Cys Gly Pro
<210> 473
<211> 22
<212> PRT
<213> Conus stercusmuscarum
<400> 473
Glx Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg Trp Cys Arg
Asp His Ser Arg Cys Cys
            20
<210> 474
<211>
      22
     PRT
<212>
     Conus consors
<213>
<400> 474
Gly Arg Cys Cys Asp Val Pro Asn Ala Cys Ser Gly Arg Trp Cys Arg
Asp His Ala Gln Cys Cys
            20
<210> 475
<211> 23
<212> PRT
<213> Conus consors
<400> 475
Glx Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
Lys Ser Leu Lys Cys Cys Ser
<210>
      476
<211> 22
<212> PRT
<213> Conus aurisiacus
<400> 476
Met Cys Cys Gly Glu Gly Arg Lys Cys Pro Ser Tyr Phe Arg Asn Ser
Gln Ile Cys His Cys Cys
            20
<210> 477
<211> 19
<212> PRT
<213> Conus aurisiacus
<400> 477
Cys Cys Arg Trp Pro Cys Pro Arg Gln Ile Asp Gly Glu Tyr Cys Gly
Cys Cys Leu
<210> 478
<211> 22
```

```
<212> PRT
<213> Conus bullatus
<400> 478
Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr Trp Lys Asn Ser
Gln Ile Cys Ala Cys Cys
<210> 479
<211> 21
<212> PRT
<213> Conus caracteristicus
<400> 479
Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Arg Asp Asn Phe
Ile Cys Gly Cys Cys
<210> 480
<211> 23
<212> PRT
<213> Conus circumcisus
<400> 480
Arg Lys Cys Cys Gly Lys Asp Gly Pro Cys Pro Lys Tyr Phe Lys Asp
Asn Phe Ile Cys Gly Cys Cys
<210> 481
<211> 20
<212> PRT
<213> Conus ermineus
<400> 481
Cys Cys Ser Trp Pro Cys Pro Arg Tyr Ser Asn Gly Lys Leu Val Cys
Phe Cys Cys Leu
<210> 482
<211>
      21
<212>
      PRT
<213>
     Conus magus
<400> 482
Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Arg Asp Asn Phe
Ile Cys Gly Cys Cys
<210>
      483
<211>
      22
<212> PRT
<213> Conus magus
<400> 483
Met Cys Cys Gly Glu Ser Ala Pro Cys Pro Ser Tyr Phe Arg Asn Ser
```

```
10
                                                         15
Gln Ile Cys His Cys Cys
            20
<210> 484
<211> 22
<212> PRT
<213> Conus magus
<400> 484
Glx Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Thr Asp
                                    10
Asn Phe Ile Cys Gly Cys
<210>
      485
<211>
       23
<212>
      PRT
<213>
     Conus magus
<400> 485
Glx Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Arg Asp
Asn Phe Ile Cys Gly Cys Cys
<210>
     486
<211> 23
<212> PRT
<213> Conus striatus
<400> 486
Glx Lys Cys Cys Gly Glu Gly Ser Ser Cys Pro Lys Tyr Phe Lys Asn
Asn Phe Ile Cys Gly Cys Cys
<210>
      487
<211>
       22
<212> PRT
<213> Conus magus
<400> 487
Glx Lys Cys Cys Ser Gly Gly Ser Cys Pro Leu Tyr Phe Arg Asp Arg
Leu Ile Cys Pro Cys Cys
            20
<210>
       488
<211>
       23
<212> PRT
<213> Conus stercusmuscarum
<400> 488
Glx Lys Cys Cys Gly Pro Gly Ala Ser Cys Pro Arg Tyr Phe Lys Asp
                                    10
Asn Phe Ile Cys Gly Cys Cys
            20
<210> 489
```

```
<211> 22
<212> PRT
<213> Conus consors
<400> 489
Met Cys Cys Gly Glu Gly Ala Pro Cys Pro Ser Tyr Phe Arg Asn Ser
Gln Ile Cys His Cys Cys
            20
<210> 490
<211> 23
<212> PRT
<213> Conus aurisiacus
<400> 490
Glx Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
Lys Asn Leu Lys Cys Cys Ser
<210> 491
<211> 23
<212> PRT
<213> Conus aurisiacus
<400> 491
Glx Lys Cys Cys Thr Gly Arg Lys Gly Ser Cys Ser Gly Lys Ala Cys
Lys Asn Leu Lys Cys Cys Ser
<210> 492
<211> 23
<212> PRT
<213> Conus bullatus
<400> 492
Val Thr Asp Arg Cys Cys Lys Gly Lys Arg Glu Cys Gly Arg Trp Cys
                                    10
Arg Asp His Ser Arg Cys Cys
            20
<210> 493
<211>
      23
<212> PRT
<213> Conus bullatus
<400> 493
Val Gly Asp Arg Cys Cys Lys Gly Lys Arg Gly Cys Gly Arg Trp Cys
Arg Asp His Ser Arg Cys Cys
            20
<210>
      494
<211>
      24
<212> PRT
<213> Conus bullatus
<400> 494
```

```
Val Gly Glu Arg Cys Cys Lys Asn Gly Lys Arg Gly Cys Gly Arg Trp
Cys Arg Asp His Ser Arg Cys Cys
            20
<210> 495
<211> 26
<212> PRT
<213> Conus bullatus
<400> 495
Ile Val Asp Arg Cys Cys Asn Lys Gly Asn Gly Lys Arg Gly Cys Ser 1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15
Arg Trp Cys Arg Asp His Ser Arg Cys Cys
       496
<210>
<211>
       25
<212> PRT
<213> Conus bullatus
<400> 496
Val Gly Cys Cys Arg Pro Lys Pro Asn Gly Gln Met Met Cys Asp Arg
Trp Cys Glu Lys Asn Ser Arg Cys Cys
<210>
      497
<211> 22
<212> PRT
<213> Conus caracteristicus
<400> 497
Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg Gln Cys Lys
Pro Gln Arg Cys Cys Ala
<210>
      498
      23
<211>
<212> PRT
<213> Conus lynceus
<400> 498
Gly Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Arg Asp Arg Ala Cys
Lys Pro Gln Arg Cys Cys Gly
<210> 499
<211>
       22
<212>
       PRT
<213> Conus lynceus
<400> 499
Glx Arg Leu Cys Cys Gly Phe Pro Lys Ser Cys Arg Ser Arg Gln Cys 1 	 10 	 15
Lys Pro His Arg Cys Cys
```

20

```
<210> 500
<211> 22
<212> PRT
<213> Conus laterculatus
<400> 500
Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Arg Asp Arg Gln Cys Lys
Pro Ala Arg Cys Cys Gly
      501
<210>
      22
<211>
<212>
      PRT
<213> Conus laterculatus
<400> 501
Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys Glu Ser Cys
Met Arg Lys Ala Cys Cys
<210> 502
<211> 22
<212> PRT
<213> Conus laterculatus
<400> 502
Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys Glu Ser Cys
Lys Arg Lys Ala Cys Cys
<210> 503
<211> 22
<212> PRT
<213> Conus geographus
<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa is Hyp
<400> 503
Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys
Xaa Gln Arg Cys Cys Ala
20
<210>
      504
      22
<211>
<212> PRT
<213> Conus geographus
<220>
<221> PEPTIDE
<222>
      (1)..(22)
<223> Xaa is Hyp
<400> 504
```

```
Arg Asp Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Arg Cys Lys
Xaa Met Lys Cys Cys Ala
<210> 505
<211> 22
<212> PRT
<213> Conus geographus
<220>
<221>
      PEPTIDE
<222>
      (1)..(22)
<223> Xaa is Hyp
<400> 505
Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Arg Cys Lys
Xaa Leu Lys Cys Cys Ala
20
<210> 506
<211> 22
<212> PRT
<213> Conus purpurascens
<220>
<221>
      PEPTIDE
<222> (1)..(22)
<223> Xaa is Hyp
<400> 506
Glx Arg Leu Cys Cys Gly Phe Xaa Lys Ser Cys Arg Ser Arg Gln Cys 1 	 10 	 15
Lys Xaa His Arg Cys Cys
<210> 507
<211>
      22
<212> PRT
<213> Conus magus
<400> 507
Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg Gln Cys Lys
Pro Gln Arg Cys Cys Ala
<210> 508
<211> 24
<212> PRT
<213> Conus marmoreus
<400> 508
Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys
Lys Pro Ala Arg Cys Cys Gly Pro
            20
<210>
       509
<211> 23
```

```
<212> PRT
<213> Conus nobilis
<400> 509
Glx Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
Lys Asn Leu Lys Cys Cys Ser
            20
<210> 510
<211> 24
<212> PRT
<213> Conus parius
<400> 510
Arg Gly Gly Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg Ala Cys
Lys Pro Ala Arg Cys Cys Gly Pro
<210> 511
<211>
      23
      PRT
<212>
<213> Conus parius
<400> 511
Arg Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys Lys
Pro Ala Arg Cys Cys Gly Pro
<210>
       512
<211> 24
<212> PRT
<213> Conus radiatus
<220>
<221>
      PEPTIDE
<222> (1)..(24)
<223> Xaa is Hyp
<400> 512
Leu Xaa Ser Cys Cys Ser Leu Asn Leu Arg Leu Cys Xaa Val Xaa Ala
Cys Lys Arg Asn Xaa Cys Cys Thr
            20
<210> 513
<211> 24
<212> PRT
<213> Conus radiatus
<220>
<221> PEPTIDE
<222>
      (1)..(24)
<223> Xaa is Hyp
<400> 513
Glx Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Xaa Val Xaa Ala Cys
```

```
Arg Ser Lys Xaa Cys Cys Lys Ser
<210> 514
<211>
      24
<212> PRT
<213> Conus radiatus
<400> 514
Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys
                                    10
Lys Pro Ala Arg Cys Cys Gly Pro
            20
<210>
      515
<211>
      23
     PRT
<212>
<213> Conus stercusmuscarum
<400> 515
Glx Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
Lys Asn Leu Lys Cys Cys Ser
            20
<210> 516
<211> 21
<212> PRT
<213> Conus tulipa
<220>
<221>
      PEPTIDE
     (1)..(21)
Xaa is Hyp
<222>
<223>
<400> 516
Xaa Gln His Cys Cys
<210> 517
<211> 21
<212> PRT
<213> Conus tulipa
<400> 517
His Gly Cys Cys Glu Gly Pro Lys Gly Cys Ser Ser Arg Glu Cys Arg 1 \phantom{000}5\phantom{000} 10 \phantom{000}15\phantom{000}
Pro Gln His Cys Cys
<210>
      518
<211> 23
<212> PRT
<213> Conus wittigi
<400> 518
Leu Pro Ser Cys Cys Asp Phe Glu Arg Leu Cys Val Val Pro Ala Cys 1 5 10 15
```

```
Ile Arg His Gln Cys Cys Thr
             20
<210> 519
<211> 17
<212> PRT
<213> Conus omaria
<400> 519
Cys Cys Lys Tyr Gly Trp Thr Cys Leu Leu Gly Cys Thr Pro Cys Asp 1 5 10 15
Cys
<210> 520
<211>
       17
<212>
        PRT
<213> Conus omaria
<400> 520
Cys Cys Arg Tyr Gly Trp Thr Cys Trp Leu Gly Cys Thr Pro Cys Gly 1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15
Cys
```